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OM protein - protein search, using sw model

Run on: June 9, 2004, 15:36:10 ; Search time 60 Seconds  
(without alignments)  
56.510 Million cell updates/sec

Title: US-09-660-302D-2  
Perfect score: 65  
Sequence: 1 DDSWVEFIELDI 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*  
1: geneseqp1980s.\*  
2: geneseqp1990s.\*  
3: geneseqp2000s.\*  
4: geneseqp2001s.\*  
5: geneseqp2002s.\*  
6: geneseqp2003as.\*  
7: geneseqp2003bs.\*  
8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	65	100.0	12	2 AAY32789	Aay32789 Growth ho
2	65	100.0	130	2 AAY32792	Aay32792 Growth ho
3	65	100.0	637	1 AAP92108	Aap92108 Human gro
4	65	100.0	638	1 AAP81326	Aap81326 Human gro
5	65	100.0	638	1 AAP81327	Aap81327 Rabbit gr
6	65	100.0	638	1 AAP92107	Aap92107 Rabbit gr
7	65	100.0	638	2 AAW33394	Aaw33394 Human gro
8	65	100.0	638	2 AAW33395	Aaw33395 Rabbit gr
9	65	100.0	638	7 ADD45061	Add45061 Rat Prote
10	65	100.0	638	7 ADD45067	Add45067 Human Pro
11	65	100.0	638	7 ADD45063	Add45063 Human Pro
12	65	100.0	638	7 ADD45065	Add45065 Rat Prote
13	65	100.0	638	4 ABB11437	Abb11437 Human gro
14	61	93.8	638	2 AAR06473	Aar06473 Serum som
15	59	90.8	12	2 AAY32794	Aay32794 Chicken G
16	59	90.8	608	2 AAR25246	Aar25246 Chickens G
17	53	81.5	12	2 AAY32793	Aay32793 Growth ho
18	48	73.8	1399	6 ABU41685	Abu41685 Protein e
19	48	73.8	1409	6 ABU39890	Abu39890 Protein e
20	45	69.2	705	5 ABB77350	Abb77350 Plodia in
21	40	61.5	193	3 AAG60096	Aag60096 Arabidops
22	40	61.5	203	3 AAG60095	Aag60095 Arabidops
23	40	61.5	251	6 ABM69113	Abm69113 Photorhab
24	40	61.5	1363	4 AAB37607	Aab37607 Human pro
25	40	61.5	1363	6 ABU04285	Abu04285 Human exp

26	39.5	60.8	300	5	ABB48962	Abb48962 Listeria
27	39	60.0	14	6	ADA09064	Ada09064 Lanthanid
28	39	60.0	163	2	AAW20448	Aaw20448 H. pylori
29	39	60.0	255	3	AAB53166	Aab53166 Macaca mu
30	39	60.0	321	2	AAB20847	Aab20847 H. pylori
31	39	60.0	404	4	ABB58263	Abb58263 Drosophil
32	39	60.0	506	7	ADC97612	Adc97612 E. faeciu
33	39	60.0	939	6	ABM70226	Abm70226 Photorhab
34	39	60.0	1023	4	ABU70491	Abu70491 Drosophil
35	39	60.0	1399	4	AAU33683	Aau33683 Pseudomon
36	39	60.0	1399	6	ABU15652	Abu15652 Protein e
37	38	58.5	103	3	AAG43966	Aag43966 Zea mays
38	38	58.5	103	3	AAG40846	Aag40846 Zea mays
39	38	58.5	133	3	AAG43965	Aag43965 Zea mays
40	38	58.5	855	5	ABP66339	Abp66339 Bifidobac
41	38	58.5	2113	7	ADC00980	Adc00980 Enterohae
42	38	58.5	3460	5	ABB05007	Abb05007 Human ree
43	38	58.5	3460	7	ADE60143	Ade60143 Human pro
44	38	58.5	3461	5	ABB05008	Abb05008 Mouse ree
45	38	58.5	3461	5	ABB57065	Abb57065 Mouse isc

ALIGNMENTS

RESULT 1

AAV32789  
ID AAV32789 standard; peptide; 12 AA.

XX AC AAY32789;

DT 09-NOV-1999 (first entry)

DE Growth hormone receptor polypeptide for inhibition of receptor cleavage.

XX Growth hormone receptor; signal transduction; proteolytic cleavage;

KW ubiquitin; proteosome binding site; muscle wasting; renal tubular defect;

KW uraemia; diabetes; Cushing's disease; eating disorder; AIDS.

OS Mammalia.

XX EP943624-A1.

XX 22-SEP-1999.

XX 12-MAR-1998; 98EP-00200799.

XX 12-MAR-1998; 98EP-00200799.

XX (UYUT-) RIJKSUNIV UTRECHT.

XX WPI; 1999-510568/43.

Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.

Claim 11; Page 27; 36pp; English.

This sequence is from the intracellular domain of the growth hormone receptor. This sequence is an example of a binding site motif AAY32790. This motif is used in a method for controlling the availability and signal transduction capability of a cell surface receptor by administering an inhibitor that is capable of inhibiting proteolytic cleavage of the receptor. Inhibition of this proteolytic cleavage results in the receptors being present on the surface for longer and therefore signalling for longer to any hormones which might be present. The binding sensitivity of cells to this sequence is an example, is located at or around a motif, of which this sequence is a complex binding site. The inhibitor ubiquitin and/or ubiquitin/proteosome complex binding site. The inhibitor of the method is either derived from, competes with, or binds to this binding motif. The inhibitor may be used to treat muscle wasting, associated with disorders such as renal tubular defects, uraemia, diabetes, Cushing's syndrome, cachexias, eating disorders, AIDS, after

CC stress and during neuromuscular disease

SQ Sequence 12 AA;

Query Match 100.0%; Score 65; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00043;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12  
|||||  
Db 1 DDSWVEFIELDI 12

RESULT 2  
AAY32792

ID AAY32792 standard; peptide; 130 AA.

XX AC AAY32792;

DT 09-NOV-1999 (first entry)

XX Growth hormone receptor polypeptide.

XX Signal transduction; proteolytic cleavage; growth hormone receptor;  
KW proteosome binding site; muscle wasting; renal tubular defect; uraemia;  
KW diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin;  
KW growth hormone deficiency.

XX OS Mammalia.

XX PN EP943624-A1.

PD 22-SEP-1999.

PF 12-MAR-1998; 98EP-00200799.

PR 12-MAR-1998; 98EP-00200799.

XX (UYUT-) RIJKSUNIV UTRECHT.

XX WPI; 1999-510568/43.

CC Controlling the availability and/or signal transduction capability of a  
PT cell surface receptor, useful for treating growth hormone deficiencies.  
XX Disclosure; Page 5; 36pp; English.

CC This sequence is a growth hormone receptor polypeptide. Polypeptides for  
CC the upregulation of the growth hormone receptor are derived from this  
CC sequence e.g. AAY32793. Variants (AAY32794-Y32823) of the derived  
CC sequence are examples of polypeptide sequences found at or near the  
CC ubiquitin/proteosome binding site located on the intracellular part of a  
CC cell surface receptor. These sequences are used in a method for  
CC controlling the availability and signal transduction capability of a cell  
CC surface receptor by administering an inhibitor that is capable of  
CC inhibiting proteolytic cleavage of the receptor. Inhibition of this  
CC proteolytic cleavage results in the receptors being present on the  
CC surface for longer and therefore signalling for longer to the interior of  
CC the cell. This increases the sensitivity of cells to any hormones which  
CC might be present. The inhibitor is either derived from, competes with or  
CC binds to a polypeptide sequence of which sequences AAY32794-Y32823 are  
CC examples. The inhibitor may be used to treat muscle wasting, associated  
CC with disorders such as renal tubular defects, uraemia, diabetes,  
CC Cushing's syndrome, cachexias, eating disorders, AIDS, after stress and  
CC during neuromuscular disease

XX Sequence 130 AA;

Query Match 100.0%; Score 65; DB 2; Length 130;  
Best Local Similarity 100.0%; Pred. No. 0.0056;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12

Db 52 DDSWVEFIELDI 63  
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RESULT 3  
AAP92108

ID AAP92108 standard; protein; 637 AA.

XX AC AAP92108;

DT 14-FEB-1990 (first entry)

XX Human growth hormone receptor.

DE Growth hormone receptor.

KW Growth hormone receptor.

XX OS Homo sapiens.

PN US4857637-A.

PD 15-AUG-1989.

XX 12-JUN-1987; 87US-00061942.

PR 22-MAY-1985; 85US-00737302.

XX 07-MAY-1986; 86US-00861236.

PA (GETH ) GENENTECH INC.

XX Hammonds RG, Leung DW, Martin DW, Spencer SA, Wood WI;

DR WPI; 1989-300419/41.

XX N-PSDB; AAN91325.

PT Modulating growth hormone receptor activity - by immunising animal  
PT against growth hormone receptor extracellular domain deriv. to raise  
PT antiserum.

PS Disclosure; Fig 2a-c; 18pp; English.

XX An animal can be immunised against its growth hormone receptor by  
CC vaccinating against a growth hormone receptor extracellular domain deriv.  
CC predetermined to raise polyclonal antisera which affect the receptor as a  
CC growth hormone agonist. This method enables continuous growth of target  
CC tissues without frequent hormone admin

SQ Sequence 637 AA;

Query Match 100.0%; Score 65; DB 1; Length 637;  
Best Local Similarity 100.0%; Pred. No. 0.031;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12  
|||||

Db 339 DDSWVEFIELDI 350

RESULT 4  
AAP81326

ID AAP81326 standard; protein; 638 AA.

XX AC AAP81326;

DT 23-OCT-1990 (first entry)

XX Human growth hormone receptor.

KW Growth hormone receptor; gigantism; acromegaly.

OS Homo sapiens.

XX Key Location/Qualifiers

PT Peptide 1.18



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QY      1 DDSWVEFIELDI 12
Db      339 DDSWVEFIELDI 350

RESULT 7
AAW333394
ID      AAW333394 standard; protein; 638 AA.
AC      AAW333394;
XX
XX      25-MAR-2003 (revised)
DT      11-MAY-1998 (first entry)
XX
XX      Human growth hormone receptor.
DE
XX      Growth hormone receptor; growth hormone binding protein; somatotropin;
KW      human; gigantism; acromegaly; therapy.
XX
XX      Homo sapiens.
OS
XX      Key      Location/Qualifiers
FH      Peptide      1..18
FT      /label= sig_peptide
FT      Domain      247..269
FT      Misc-difference 375
FT      /note= "transmembrane domain"
FT      /note= "translated codon is Ser in clone ghr.210 and
FT      ghr.110, Ile in ghr.501"
PN      US5688763-A.
XX
XX      18-NOV-1997.
PD
XX
XX      25-MAY-1994; 94US-00248832.
PF
XX      12-JUN-1987; 87US-00062542.
PR      28-JUN-1991; 91US-00723358.
PR      08-JAN-1993; 93US-00002489.
XX
XX      (LEUN/) LEUNG D W.
PA      (HAMM/) HAMMONDS R G.
PA      (WOOD/) WOOD W I.
PA      (COLO/) COLOSI P C.
PA      (SPEN/) SPENCER S A.
XX
XX      Colosi PC, Spencer SA, Leung DW, Hammonds RG, Wood WI;
PI      WPI; 1998-008010/01.
XX      N-PSDB; AAT94063.
DR
XX
XX      Human and rabbit growth hormone receptor protein - useful to treat
FT      disorders associated with overexpression, e.g. gigantism and acromegaly.
XX
XX      Claim 2; Fig 8a; 60pp; English.
PS
XX
XX      This protein sequence comprises human growth hormone receptor. The amino
CC      acid sequence was deduced from cDNA clones (see AAT94063) obtained from a
CC      human liver cDNA library, and shows 84% identity to the rabbit growth
CC      hormone receptor (see AAW333395). Human growth hormone receptor, its
CC      derivatives in which the cytoplasmic or transmembrane domains are
CC      deleted, and growth hormone binding proteins comprising amino acids 190-
CC      246 or 1-324 of the mature protein, can be used to treat disorders
CC      associated with growth hormone over-expression, e.g. gigantism and
CC      acromegaly. The binding protein may also be used to increase the
CC      stability and efficacy of growth hormone in vivo. (Updated on 25-MAR-2003
CC      to correct PF field.)
XX
XX      Sequence 638 AA;
SQ
Query Match      100.0%; Score 65; DB 2; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 DDSWVEFIELDI 12
Db      339 DDSWVEFIELDI 350

RESULT 8
AAW333395
ID      AAW333395 standard; protein; 638 AA.
AC      AAW333395;
XX
XX      25-MAR-2003 (revised)
DT      11-MAY-1998 (first entry)
XX
XX      Rabbit growth hormone receptor.
DE
XX      Growth hormone receptor; growth hormone binding protein; somatotropin;
KW      rabbit; gigantism; acromegaly; therapy.
XX
XX      Oryctolagus cuniculus.
OS
XX      Key      Location/Qualifiers
FH      Peptide      1..18
FT      /label= Sig_peptide
FT      Misc-difference 49
FT      /note= "translated codon is Ala in clone ghr.435, Thr in
FT      ghr.440"
FT      247..269
FT      /note= "transmembrane domain"
PN      US5688763-A.
XX
XX      18-NOV-1997.
PD
XX
XX      25-MAY-1994; 94US-00248832.
PF
XX      12-JUN-1987; 87US-00062542.
PR      28-JUN-1991; 91US-00723358.
PR      08-JAN-1993; 93US-00002489.
XX
XX      (LEUN/) LEUNG D W.
PA      (HAMM/) HAMMONDS R G.
PA      (WOOD/) WOOD W I.
PA      (COLO/) COLOSI P C.
PA      (SPEN/) SPENCER S A.
XX
XX      Colosi PC, Spencer SA, Leung DW, Hammonds RG, Wood WI;
PI      WPI; 1998-008010/01.
XX      N-PSDB; AAT94064.
DR
XX
XX      Human and rabbit growth hormone receptor protein - useful to treat
FT      disorders associated with overexpression, e.g. gigantism and acromegaly.
XX
XX      Claim 2; Fig 8b; 60pp; English.
PS
XX
XX      This protein sequence comprises rabbit growth hormone receptor. The amino
CC      acid sequence was deduced from cDNA clones (see AAT94064) obtained from a
CC      rabbit liver cDNA library, and shows 84% identity to the human growth
CC      hormone receptor (see AAW33394). Rabbit and human growth hormone
CC      receptors, their derivatives in which the cytoplasmic or transmembrane
CC      domains are deleted, and growth hormone binding proteins comprising amino
CC      acids 190-246 or 1-324 of the mature proteins, can be used to treat
CC      disorders associated with growth hormone over-expression, e.g. gigantism
CC      and acromegaly. The binding protein may also be used to increase the
CC      stability and efficacy of growth hormone in vivo. (Updated on 25-MAR-2003
CC      to correct PF field.)
XX
XX      Sequence 638 AA;
SQ
Query Match      100.0%; Score 65; DB 2; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.031;

```

SQ Sequence 638 AA;  
 Query Match 100.0%; Score 65; DB 7; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 0.031;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12  
 |||||  
 Db 340 DDSWVEFIELDI 351

RESULT 10  
 ADD45067  
 ID ID ADD45067 standard; protein; 638 AA.  
 XX AC AC  
 XX ADD45067;  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human Protein P10912, SEQ ID NO 10499.  
 XX  
 KW Human; pain; neuronal tissue; gene therapy;  
 KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 KW spared nerve injury; SNI; Chung.  
 XX  
 OS Homo sapiens.  
 OS  
 PN WO2003016475-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 14-AUG-2002; 2002WO-US025765.  
 XX  
 PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX  
 XX Woolf C, D'urso D, Befort K, Costigan M;  
 PI  
 DR WPI; 2003-268312/26.  
 DR GENBANK; P10912.  
 XX  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 PS Claim 1; Page; 1017pp; English.  
 XX  
 CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 638 AA;

Query Match 100.0%; Score 65; DB 7; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 0.031;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIEDI 12  
 |||||  
 Db 339 DDSWVEFIEDI 350

RESULT 11

ADD45063  
 ID ADD45063 standard; protein; 638 AA.

XX AC ADD45063;

XX DT 29-JAN-2004 (first entry)

XX DE Human Protein P10912, SEQ ID NO 10495.

XX KW Human; pain; neuronal tissue; gene therapy;

XX KW spinal segmental nerve injury; chronic constriction injury; CCI;  
 XX KW spared nerve injury; SNI; Chung.

XX OS Homo sapiens.

XX FN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO ) GEN HOSPITAL CORP.

XX PA (FARB ) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR WPI; 2003-268312/26.

XX DR GENBANK; P10912.

XX PT New composition comprising two or more isolated polypeptides, useful for  
 XX preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat  
 XX or human polynucleotides or a polynucleotide which represents a fragment,  
 XX derivative or allelic variation of the nucleic acid sequence. Also  
 XX claimed are a vector comprising the novel polynucleotide, a host cell  
 XX comprising the vector, a method for identifying a nucleotide sequence  
 XX which is differentially regulated in an animal subjected to pain and a  
 XX kit to perform the method, an array, a method for identifying an agent  
 XX that increases or decreases the expression of the polynucleotide sequence  
 XX that is differentially expressed in neuronal tissue of a first animal  
 XX subjected to pain, a method for identifying a compound which regulates  
 XX the expression of a polynucleotide sequence which is differentially  
 XX expressed in an animal subjected to pain, a method for identifying a  
 XX compound that regulates the activity of one or more of the  
 XX polynucleotides, a method for producing a pharmaceutical composition, a  
 XX method for identifying a compound or small molecule that regulates the  
 XX activity in an animal of one or more of the polypeptides given in the  
 XX specification, a method for identifying a compound useful in treating  
 XX pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 638 AA;

Query Match 100.0%; Score 65; DB 7; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 0.031;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIEDI 12  
 |||||  
 Db 339 DDSWVEFIEDI 350

RESULT 12

ADD45065  
 ID ADD45065 standard; protein; 638 AA.

XX AC ADD45065;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein P16310, SEQ ID NO 10497.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX FN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO ) GEN HOSPITAL CORP.

XX PA (FARB ) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX DR WPI; 2003-268312/26.

XX DR GENBANK; P16310.

XX PT New composition comprising two or more isolated polypeptides, useful for  
 XX preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat  
 XX or human polynucleotides or a polynucleotide which represents a fragment,  
 XX derivative or allelic variation of the nucleic acid sequence. Also  
 XX claimed are a vector comprising the novel polynucleotide, a host cell  
 XX comprising the vector, a method for identifying a nucleotide sequence  
 XX which is differentially regulated in an animal subjected to pain and a  
 XX kit to perform the method, an array, a method for identifying an agent  
 XX that increases or decreases the expression of the polynucleotide sequence  
 XX that is differentially expressed in neuronal tissue of a first animal  
 XX subjected to pain, a method for identifying a compound which regulates  
 XX the expression of a polynucleotide sequence which is differentially  
 XX expressed in an animal subjected to pain, a method for identifying a  
 XX compound that regulates the activity of one or more of the  
 XX polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Seq Sequence 638 AA;

Query Match 100.0%; Score 65; DB 7; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 0.031;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12  
 |||||  
 Db 340 DDSWVEFIELDI 351

RESULT 13

ID ABB11437 standard; peptide; 648 AA.

XX AC ABB11437;

DT 11-JAN-2002 (first entry)

XX Human growth hormone receptor homologue, SEQ ID NO:1807.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor;  
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;  
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KW chronic inflammatory condition; proliferative retinopathy;  
 KW atherosclerosis; coronary heart disease; arterial ischaemia;  
 KW bone disorder; osteoporosis; vascular growth disorder;  
 KW tissue regeneration; wound healing; infection; immune disorder;  
 KW cell culture; drug screening; gene therapy; antiinflammatory;  
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;  
 KW antifungal; vulnery; antiulcer.

XX Homo sapiens.

XX WO200157188-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US003800.

XX 03-FEB-2000; 2000US-00496914.

XX 27-APR-2000; 2000US-00560875.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-457740/49.

XX N-PSDB; ABA08681.

XX Human proteins and DNA encoding sequences useful for preventing, treating  
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis  
 PT and cancer.

PS Claim 20; Page 189-190; 1963pp; English.

CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides,  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth factor activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a novel human  
 CC polypeptide of the invention

XX Seq Sequence 648 AA;

Query Match 100.0%; Score 65; DB 4; Length 648;  
 Best Local Similarity 100.0%; Pred. No. 0.031;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12  
 |||||  
 Db 349 DDSWVEFIELDI 360

RESULT 14

XX AAR06473

ID AAR06473 standard; protein; 638 AA.

XX AC AAR06473;

XX 27-AUG-2003 (revised)  
 DT 04-JAN-1991 (first entry)

XX Serum somatotropin receptor protein from clone PRAT7-12.

DE Somatotropin receptor; SR; somatotropin binding protein; SBP; PRAT7-12;  
 KW PRAT1-6.

XX Rattus rattus.

XX Key Location/Qualifiers  
 FH Peptide 1..17

FT /label= signal\_sequence  
 FT 262..638

FT /label= divergence

FT /note= "non-homology region with SBP/pRTA1-6"  
 FT 264..289

FT Domain /label= transmembrane\_domain

```

XX PN EP383205-A.
XX PD 22-AUG-1990.
XX PF 09-FEB-1990; 90EP-00102552.
XX PR 17-FEB-1989; 89US-00310725.
XX PA (AMCY ) AMERICAN CYANAMID CO.
XX PI Logan JS, Baumbach WR;
XX DR WPI; 1990-255493/34.
XX DR N-PSDB; AAQ05691.
XX PS
XX PT Somatotropin binding protein and gene - used to regulate and/or modify
XX PT activity of somatotropin in humans and animals.
XX PS Disclosure; Fig 6; 43pp; English.
XX CC Homology comparison between this putative rat somatotropin receptor and
XX CC the published sequence indicates 70% identity. See also AAQ05689-91,
XX CC AAQ06124 and AAQ05700. (Updated on 27-AUG-2003 to correct OS field.)
XX SQ
SQ Sequence 638 AA;
Query Match 93.8%; Score 61; DB 2; Length 638;
Best Local Similarity 91.7%; Pred. No. 0.14;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12
Db 340 DESWVEFIELDI 351
|:|||||

RESULT 15
AAQ32794
ID AAQ32794 standard; peptide; 12 AA.
XX AC
XX AC AAQ32794;
XX DT
XX DT 09-NOV-1999 (first entry)
XX DE
XX DE Chicken growth hormone receptor derived polypeptide.
XX KW Signal transduction; proteolytic cleavage; growth hormone receptor;
XX KW proteosome binding site; muscle wasting; renal tubular defect; uraemia;
XX KW diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin;
XX KW growth hormone deficiency; inhibitor.
XX OS
XX OS Gallus gallus.
XX PN
XX PN EP943624-A1.
XX PD
XX PD 22-SEP-1999.
XX PF
XX PF 12-MAR-1998; 98EP-00200799.
XX PR
XX PR 12-MAR-1998; 98EP-00200799.
XX PA
XX PA (UYUT-) RIJKSUNIV UTRECHT.
XX DR
XX DR WPI; 1999-510568/43.
XX PT
XX PT Controlling the availability and/or signal transduction capability of a
XX PT cell surface receptor, useful for treating growth hormone deficiencies.
XX PS
XX PS Disclosure; Page 9; 36pp; English.
XX CC
XX CC This sequence is a polypeptide from the chicken growth hormone receptor.
XX CC Sequences (AAQ32794-Y32823) are examples of polypeptide sequences found
XX CC at or near the ubiquitin/proteosome complex binding site located on the

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```

CC intracellular part of a cell surface receptor. These sequences are used
CC in a method for controlling the availability and signal transduction
CC capability of a cell surface receptor by administering an inhibitor that
CC is capable of inhibiting proteolytic cleavage of the receptor. Inhibition
CC of this proteolytic cleavage results in the receptors being present on
CC the surface for longer and therefore signalling for longer to the
CC interior of the cell. This increases the sensitivity of cells to any
CC hormones which might be present. The inhibitor is either derived from,
CC competes with or binds to a polypeptide sequence of which sequences
CC AAQ32794-Y32823 are examples. The inhibitor may be used to treat muscle
CC wasting, associated with disorders such as renal tubular defects,
CC uraemia, diabetes, Cushing's syndrome, cachexias, eating disorders, AIDS,
CC after stress and during neuromuscular disease
XX SQ
SQ Sequence 12 AA;

```

```

Query Match 90.8%; Score 59; DB 2; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0041;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

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QY 1 DDSWVEFIELDI 12
Db 1 DDLWVEFIELDI 12
|:|||||

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Search completed: June 9, 2004, 15:48:26
Job time : 62 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 9, 2004, 15:43:40 ; Search time 13.2973 Seconds  
(without alignments)  
86.807 Million cell updates/sec

Title: US-09-660-302D-2

Perfect score: 65

Sequence: 1 DDSWVEFIELDI 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	65	100.0	634	2 S33339	somatotropin recep
2	65	100.0	638	2 A33505	somatotropin recep
3	65	100.0	638	2 A33991	somatotropin recep
4	65	100.0	638	2 B28176	somatotropin recep
5	65	100.0	638	2 S12136	somatotropin recep
6	65	100.0	677	2 S33608	somatotropin-bind
7	59	90.8	608	2 S32823	somatotropin recep
8	48	73.8	702	2 A61619	arylphorin precurs
9	43	66.2	411	2 S66916	hypothetical prote
10	43	66.2	704	2 A34287	storage protein 2
11	41	63.1	1379	2 JC4954	vascular endotheli
12	40	61.5	442	2 AD2113	hypothetical prote
13	40	61.5	1363	2 I58375	protein-tyrosine k
14	39.5	60.8	300	2 AF1115	transcription regu
15	39.5	60.8	300	2 AG1476	signal recognition
16	39	60.0	103	2 T03951	hypothetical prote
17	39	60.0	217	2 AG2426	probable 3-oxoacyl
18	39	60.0	264	1 E70027	hypothetical prote
19	39	60.0	321	2 H71924	hypothetical prote
20	39	60.0	321	2 B64589	hypothetical prote
21	39	60.0	829	2 T19514	hypothetical prote
22	39	60.0	1399	2 G83112	DNA-directed RNA p
23	38	58.5	363	2 S75238	hypothetical prote
24	38	58.5	489	2 T27468	hypothetical prote
25	38	58.5	698	1 S00742	cytochrome-c oxida
26	38	58.5	2113	2 G91286	probable RNA helic
27	38	58.5	2113	2 C86128	probable helicase
28	38	58.5	3461	2 S58870	reelin precursor -
29	37.5	57.7	3707	2 S18252	heparan sulfate pr

30	37.5	57.7	4391	2 A38096	perlecan precursor
31	37	56.9	190	2 AI3299	5-methylcytosine-s
32	37	56.9	198	2 E70357	conserved hypothet
33	37	56.9	258	2 S74631	hypothetical prote
34	37	56.9	339	1 NCBPX4	exonuclease 47 (EC
35	37	56.9	436	2 D64028	hypothetical prote
36	37	56.9	457	2 G69341	conserved hypothet
37	37	56.9	473	2 C96516	Fl6N3.15 [imported
38	37	56.9	595	2 AF2097	hypothetical prote
39	37	56.9	648	2 T09036	hypothetical prote
40	37	56.9	804	2 A39972	segment S5 protein
41	37	56.9	840	2 T36175	probable large ATP
42	37	56.9	1263	2 T13805	spalt-related prot
43	37	56.9	1298	2 A48999	protein-tyrosine k
44	36.5	56.2	355	2 S18510	MATa1 splicing fac
45	36.5	56.2	1107	2 S61667	probable membrane

ALIGNMENTS

RESULT 1

S33339

somatotropin receptor - sheep

N;Alternate names: growth hormone receptor

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 08-Dec-1993 #sequence\_revision 01-Dec-1995 #text\_change 02-Aug-2002

C;Accession: S33339

R;Adams, T.E.; Baker, L.; Fiddes, R.J.; Brandon, M.R.

Mol. Cell. Endocrinol. 73, 135-145, 1990

A;Title: The sheep growth hormone receptor: molecular cloning and ontogeny of mRNA expr

A;Reference number: S33339; MUID:91099608; PMID:1980117

A;Accession: S33339

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-634 <ADA>

A;Cross-references: EMBL:M82912; NID:g165888; PIDN:AAA73171.1; PID:g165889

C;Superfamily: Interleukin-2 receptor beta chain; fibronectin type III repeat homology

Query Match 100.0%; Score 65; DB 2; Length 634;

Best Local Similarity 100.0%; Pred. No. 0.0037;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12

|||||

Db 335 DDSWVEFIELDI 346

RESULT 2

A33505

somatotropin receptor precursor - rat

N;Alternate names: growth hormone receptor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Nov-1989 #sequence\_revision 22-Nov-1989 #text\_change 02-Aug-2002

C;Accession: A32985; A33505

R;Baumbach, W.R.; Horner, D.L.; Logan, J.S.

Genes Dev. 3, 1199-1205, 1989

A;Title: The growth hormone-binding protein in rat serum is an alternatively spliced for

A;Reference number: A32985; MUID:9006741; PMID:2792761

A;Accession: A32985

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-638 <BAU>

A;Cross-references: GB:X16726

R;Mathews, L.S.; Enberg, B.; Norstedt, G.

J. Biol. Chem. 264, 9905-9910, 1989

A;Title: Regulation of rat growth hormone receptor gene expression.

A;Reference number: A33505; MUID:89255563; PMID:2722883

A;Accession: A33505

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-638 <MAT>

A;Cross-references: GB:J04811; NID:g204308; PIDN:AAA41219.1; PID:g204309

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology  
C;Keywords: transmembrane protein

Query Match 100.0%; Score 65; DB 2; Length 638;  
Best Local Similarity 100.0%; Pred. No. 0.0037;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12  
|||||  
Db 340 DDSWVEFIELDI 351

## RESULT 3

A33991  
somatotropin receptor precursor - human  
N;Alternate names: growth hormone receptor  
N;Contains: somatotropin-binding protein, serum  
C;Species: Homo sapiens (man)  
C;Date: 23-Mar-1990 #sequence\_revision 23-Mar-1990 #text\_change 02-Aug-2002  
C;Accession: A33991; S04530  
R;Godowski, P.J.; Leung, D.W.; Meacham, L.R.; Galgani, J.P.; Hellmiss, R.; Keret, R.; R  
Proc. Natl. Acad. Sci. U.S.A. 86, 8083-8087, 1989  
A;Title: Characterization of the human growth hormone receptor gene and demonstration of  
A;Reference number: A33991; MUID:90046742; PMID:2813379  
A;Accession: A33991  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-638 <GOD>  
A;Cross-references: GB:M28458; GB:M28459; GB:M28460; GB:M28461; GB:M28462; GB:M28463; GB  
R;Leung, D.W.; Spencer, S.A.; Cachianes, G.; Hammonds, R.G.; Collins, C.; Henzel, W.J.;  
Nature 330, 537-543, 1987  
A;Title: Growth hormone receptor and serum binding protein: purification, cloning and ex  
A;Reference number: S04530; MUID:88065896; PMID:2825030  
A;Accession: S04530  
A;Molecule type: mRNA  
A;Residues: 1-543, '1', 545-638 <LEU>  
A;Cross-references: EMBL:X06562; NID:g31737; PIDN:CAA29808.1; PID:g31738  
C;Genetics:  
A;Gene: GDB:GHR  
A;Cross-references: GDB:l19984; OMIM:600946  
A;Map Position: Spl3-Spl2  
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology  
C;Keywords: liver; transmembrane protein  
F;1-18/Domain: signal sequence #status predicted <SIG>  
F;19-638/Product: somatotropin receptor #status predicted <MAT>  
F;265-288/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 65; DB 2; Length 638;  
Best Local Similarity 100.0%; Pred. No. 0.0037;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12  
|||||  
Db 339 DDSWVEFIELDI 350

## RESULT 4

B28176  
somatotropin receptor precursor, hepatic - rabbit  
N;Alternate names: growth hormone receptor  
N;Contains: somatotropin-binding protein, serum  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 28-Feb-1990 #sequence\_revision 10-Mar-1994 #text\_change 02-Aug-2002  
C;Accession: S08544; A28176  
R;Leung, D.W.; Spencer, S.A.; Cachianes, G.; Hammonds, R.G.; Collins, C.; Henzel, W.J.;  
Nature 330, 537-543, 1987  
A;Title: Growth hormone receptor and serum binding protein: purification, cloning and ex  
A;Reference number: S04530; MUID:88065896; PMID:2825030  
A;Accession: S08544  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-638 <LEU>  
A;Cross-references: GB:AF015252; NID:g2342651; PIDN:AA867613.1; PID:g2342652

A;Note: part of this sequence, including the amino end of the mature protein, was confi  
R;Spencer, S.A.; Hammonds, R.G.; Henzel, W.J.; Rodriguez, H.; Waters, M.J.; Wood, W.I.  
J. Biol. Chem. 263, 7862-7867, 1988

A;Title: Rabbit liver growth hormone receptor and serum binding protein. Purification,  
A;Reference number: A92721; MUID:88227992; PMID:3372509

A;Accession: B28176

A;Molecule type: protein

A;Residues: 19-34; 'SPG', 81-88; 'X', 99, 'XX', 102-105, 'X', 107-110, 'XX', 113-114, 'X', 141, 'X',  
-574, 'X', 576-577; 579-595 <SPE>

A;Note: sequence is derived from intact receptor

A;Accession: A28176

A;Molecule type: protein

A;Residues: 'XXX', 22-45, 'X', 47-55 <SP2>

A;Note: sequence is derived from a soluble form of the receptor isolated from serum  
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

C;Keywords: glycoprotein; liver; transmembrane protein

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-638/Product: somatotropin receptor #status experimental <MAT>

F;265-288/Domain: transmembrane #status predicted <TMM>

F;46, 200/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 65; DB 2; Length 638;  
Best Local Similarity 100.0%; Pred. No. 0.0037;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12  
|||||  
Db 339 DDSWVEFIELDI 350

## RESULT 5

S12136  
somatotropin receptor precursor - pig  
N;Alternate names: growth hormone receptor  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 02-Aug-2002  
C;Accession: S12136  
R;Cioffi, J.A.; Wang, X.; Kopchick, J.J.  
Nucleic Acids Res. 18, 6451, 1990  
A;Title: Porcine growth hormone receptor cDNA sequence.  
A;Reference number: S12136; MUID:91057155; PMID:2243805  
A;Accession: S12136  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-638 <CIO>  
A;Cross-references: EMBL:X54429; NID:g2037; PIDN:CAA38301.1; PID:g2038  
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology  
C;Keywords: transmembrane protein

Query Match 100.0%; Score 65; DB 2; Length 638;  
Best Local Similarity 100.0%; Pred. No. 0.0037;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12  
|||||  
Db 339 DDSWVEFIELDI 350

## RESULT 6

S33608  
somatotropin-binding protein, high molecular weight, precursor - mouse  
N;Alternate names: growth hormone-binding protein, high molecular weight  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 02-Aug-2002  
C;Accession: S33608; S33607  
R;Smith, W.C.; Kuniyoshi, J.; Talamantes, F.  
Mol. Endocrinol. 3, 984-990, 1989  
A;Title: Mouse serum growth hormone (GH) binding protein has GH receptor extracellular  
A;Reference number: S33607; MUID:89295449; PMID:2739661  
A;Accession: S33608  
A;Molecule type: mRNA  
A;Residues: 1-677 <SMI>  
A;Cross-references: EMBL:M33324; NID:g193508; PIDN:AAA37690.1; PID:g309253

A;Experimental source: liver

A;Accession: S33607

A;Molecule type: mRNA

A;Residues: 1-324 <SM2>

A;Cross-references: EMBL:M31680; NID:g193506; PIDN:AAA37689.1; PID:g309252

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

C;Keywords: glycoprotein; receptor; transmembrane protein

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-677/Product: somatotropin-binding protein, high molecular weight #status predicted

F;274-297/Domain: transmembrane #status predicted <TM>

F;40,164,169/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;164,169/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 100.0%; Score 65; DB 2; Length 677;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12

|||||

Db 375 DDSWVEFIELDI 386

RESULT 7

S32823

somatotropin receptor precursor, major splice form - chicken

N;Alternate names: growth hormone receptor

N;Contains: somatotropin receptor, short form

C;Species: Gallus gallus (chicken)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 02-Aug-2002

C;Accession: S32823; A49812

R;Burnside, J.; Liou, S.S.; Cogburn, L.A.

Endocrinology 128, 3183-3192, 1991

A;Title: Molecular cloning of the chicken growth hormone receptor complementary deoxyrib

A;Reference number: S32823; MUID:91243665; PMID:2036984

A;Accession: S32823

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-608 <BUR>

A;Cross-references: EMBL:M74057; NID:g211810; PIDN:AAA48781.1; PID:g211811

R;Huang, N.; Cogburn, L.A.; Agarwal, S.K.; Marks, H.L.; Burnside, J.

Mol. Endocrinol. 7, 1391-1398, 1993

A;Title: Overexpression of a truncated growth hormone receptor in the sex-linked dwarf c

A;Reference number: A49812; MUID:94158898; PMID:8114754

A;Accession: A49812

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-109 <HUA>

A;Cross-references: GB:S68576; NID:g499137; PIDN:AAB29983.1; PID:g499138

A;Experimental source: liver, normal chicken

A;Note: this truncated form is a minor splice form in normal chickens and the major form

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

C;Keywords: alternative splicing; receptor; sex-linked inheritance; transmembrane protei

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-109/Product: somatotropin receptor, short form #status predicted <SHO>

Query Match

Best Local Similarity 90.8%; Score 59; DB 2; Length 608;

Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12

|||||

Db 312 DDSWVEFIELDI 323

RESULT 8

A61619

arylphorin precursor - greater wax moth

N;Alternate names: phenylalanine-rich protein lhp76

C;Species: Galleria mellonella (greater wax moth)

C;Date: 21-Jul-1995 #sequence\_revision 11-Aug-1995 #text\_change 24-Sep-1999

C;Accession: A61619

R;Mammel, N.A.; Trewitt, P.M.; Silhacek, D.L.; Kumaran, A.K.

Insect Biochem. Mol. Biol. 22, 333-342, 1992

A;Title: Nucleotide sequence and structure of the arylphorin gene from Galleria mellonella

A;Reference number: A61619

A;Accession: A61619

A;Molecule type: DNA

A;Residues: 1-702 <MEM>

A;Cross-references: GB:M73793; NID:g159077; PIDN:AAA74229.1; PID:g159078

A;Note: in the authors' translation, residue 306-Leu is omitted, residue 317-Asn is dupl

C;Genetics:

A;Introns: 30/1; 74/3; 352/3; 410/2

A;Note: single copy gene

C;Superfamily: arylphorin

C;Keywords: glycoprotein; hemolymph; storage protein

F;1-16/Domain: signal sequence #status predicted <SIG>

F;211,481/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 73.8%; Score 48; DB 2; Length 702;

Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 11

|||||

Db 546 EDWINFIELD 556

RESULT 9

S66916

hypothetical protein YOR042w - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein O2762

C;Species: Saccharomyces cerevisiae

C;Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 19-Apr-2002

C;Accession: S66916

R;Landt, O.; Hiesel, R.; Unseld, M.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S66907

A;Accession: S66916

A;Molecule type: DNA

A;Residues: 1-411 <LAN>

A;Cross-references: EMBL:Z74949; NID:g1420165; PID:e251966; PID:g1420167; GSPDB:GN00015

A;Experimental source: strain S288C

C;Genetics:

A;Gene: MIPS:YOR042w

A;Cross-references: SGD:S0005568

A;Map position: 15R

Query Match

Best Local Similarity 66.2%; Score 43; DB 2; Length 411;

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12

|||||

Db 223 EDSWSQFVEKDL 234

RESULT 10

A34287

storage protein 2 - silkworm

C;Species: Bombyx mori (silkworm)

C;Date: 08-Jun-1990 #sequence\_revision 08-Jun-1990 #text\_change 04-Sep-1998

C;Accession: A34287

R;Fujii, T.; Sakurai, H.; Izumi, S.; Tomino, S.

J. Biol. Chem. 264, 11020-11025, 1989

A;Title: Structure of the gene for the arylphorin-type storage protein SP 2 of Bombyx mo

A;Reference number: A34287; MUID:89291839; PMID:2544581

A;Accession: A34287

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-704 <FUJ>

C;Superfamily: arylphorin

Query Match

Best Local Similarity 66.2%; Score 43; DB 2; Length 704;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDSWVEFIELD 11  
:|:|:|  
Db 543 EDNWKFFELD 553

## RESULT 11

JC4954  
vascular endothelial growth factor receptor 2 precursor - Japanese quail  
N;Alternate names: Quail endothelial kinase 2; Quek 2  
C;Species: Coturnix coturnix japonica (Japanese quail)  
C;Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 24-Sep-1999  
C;Accession: JC4954  
R;Eichmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.  
Gene 174, 3-8, 1996  
A;Title: Molecular cloning of Quek 1 and 2, two quail vascular endothelial growth factor  
A;Reference number: JC4953; MUID:97017121; PMID:8863722  
A;Accession: JC4954  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-1379 <EIC>  
A;Cross-references: EMBL:X83287; NID:q619865; PIDN:CAA58267.1; PID:e283815; PID:q1707416  
C;Comment: This protein is an endothelial-specific receptor and binds vascular endothelial  
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol  
C;Keywords: ATP; embryo; growth factor receptor; transmembrane protein  
F;1-207/Domain: signal sequence #status predicted <SIG>  
F;789-810/Domain: transmembrane #status predicted <TM>  
F;856-1188/Domain: protein kinase homology <KIN>  
F;864-872/Region: protein kinase ATP-binding motif

Query Match 63.1%; Score 41; DB 2; Length 1379;  
Best Local Similarity 75.0%; Pred. No. 97;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DSWVEFIE 9  
|:|:|:|:|

Db 519 DTWVEFVE 526

## RESULT 12

AD2113  
hypothetical protein all2459 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C;Accession: AD2113  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriquchi  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AD2113  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-442 <KUR>  
A;Cross-references: GB:BA000019; PIDN:BA074158.1; PID:g17131551; GSPDB:GN00179  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: all2459

Query Match 61.5%; Score 40; DB 2; Length 442;  
Best Local Similarity 60.0%; Pred. No. 43;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDSWVEFIEL 10  
|:|:|:|:|

Db 225 DDSWDYDIKL 234

## RESULT 13

I58375  
protein-tyrosine kinase (EC 2.7.1.112) flt4 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 04-Feb-2000

C;Accession: I58375; B42010  
R;Finnerty, H.; Kelleher, K.; Morris, G.E.; Bean, K.; Merberg, D.M.; Kriz, R.; Morris,  
Oncogene 8, 2293-2298, 1993  
A;Title: Molecular cloning of murine FLT and FLT4.  
A;Reference number: I58375; MUID:93330572; PMID:8393164  
A;Accession: I58375  
A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA  
A;Residues: 1-1363 <RES>  
A;Cross-references: GB:I07296; NID:g293780; PIDN:AAA40077.1; PID:g293781  
R;Galland, F.; Karamysheva, A.; Mattei, M.G.; Rosnet, O.; Marchetto, S.; Birnbaum, D.  
Genomics 13, 475-478, 1992  
A;Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene.  
A;Reference number: A42010; MUID:92307693; PMID:1319394  
A;Accession: B42010  
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr  
A;Molecule type: DNA  
A;Residues: 1033-1072 <GAL>  
C;Genetics:  
A;Gene: FLT4

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol  
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase  
F;843-1176/Domain: protein kinase homology <KIN>  
F;851-859/Region: protein kinase ATP-binding motif

Query Match 61.5%; Score 40; DB 2; Length 1363;  
Best Local Similarity 75.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DSWVEFIE 9  
|:|:|:|:|

Db 505 DSWTEFVE 512

## RESULT 14

AF1115  
transcription regulators homolog lmo0325 [imported] - Listeria monocytogenes (strain EGD  
C;Species: Listeria monocytogenes  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C;Accession: AF1115  
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke  
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H  
Science 294, 849-852, 2001  
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M  
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland  
A;Title: Comparative genomics of Listeria species.  
A;Reference number: AB1077; MUID:21537279; PMID:11679669  
A;Accession: AF1115  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-300 <GLA>  
A;Cross-references: GB:NC\_003210; PIDN:CAD00852.1; PID:g16409689; GSPDB:GN00177  
A;Experimental source: strain EGD-e  
C;Genetics:  
A;Gene: lmo0325

Query Match 60.8%; Score 39.5; DB 2; Length 300;  
Best Local Similarity 63.6%; Pred. No. 34;  
Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 DDSWVEFIEL 10  
|:|:|:|:|

Db 73 DDSFWIDFVEL 83

## RESULT 15

AG1476

transcription regulators homolog lin0350 [imported] - Listeria innocua (strain Clip1126)  
C;Species: Listeria innocua  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C;Accession: AG1476  
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker

.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A;Title: Comparative genomics of *Listeria* species.  
A;Reference number: AB1077; MUID:21537279; PMID:11679669  
A;Accession: AG1476  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-300 <GLA>  
A;Cross-references: GB:AL592022; PIDN:CAC95583.1; PID:g16412779; GSPDB:GN00178  
A;Experimental source: strain Clip11262  
C;Genetics:  
A;Gene: lin0350

Query Match 60.8%; Score 39.5; DB 2; Length 300;  
Best Local Similarity 63.6%; Pred.No. 34;  
Matches 7; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 DDS-WVEFIEL 10  
Db 73 DDSFWIDFVEL 83

Search completed: June 9, 2004, 15:52:16  
Job time : 14.2973 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 9, 2004, 15:36:55 ; Search time 8.75676 Seconds

(without alignments)

71.355 Million cell updates/sec

Title: US-09-660-302D-2

Perfect score: 65

Sequence: 1 DDSWVEFIELDI 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	634	1	GHR_BOVIN
2	65	100.0	634	1	GHR_SHEEP
3	65	100.0	638	1	GHR_HUMAN
4	65	100.0	638	1	GHR_MACMU
5	65	100.0	638	1	GHR_PIG
6	65	100.0	638	1	GHR_RABIT
7	65	100.0	638	1	GHR_RAT
8	65	100.0	650	1	GHR_MOUSE
9	59	90.8	608	1	GHR_CHICK
10	59	90.8	611	1	GHR_COLLI
11	48	73.8	1409	1	RPOC_PSEPU
12	43	66.2	704	1	SSP2_BOMMO
13	40	61.5	358	1	Y4FP_RHISN
14	40	61.5	1363	1	VGR3_MOUSE
15	39	60.0	103	1	SR09_MAIZE
16	39	60.0	1399	1	RPOC_PSEAE
17	38	58.5	698	1	COX1_TETPY
18	38	58.5	3460	1	RELN_HUMAN
19	38	58.5	3461	1	RELN_MOUSE
20	38	58.5	3462	1	RELN_RAT
21	37.5	57.7	3707	1	PGBM_MOUSE
22	37.5	57.7	4391	1	PGBM_HUMAN
23	37	56.9	173	1	GLBC_NIPBR
24	37	56.9	339	1	EX01_EPT4
25	37	56.9	341	1	MURB_SHECN
26	37	56.9	436	1	YEO9_HAEIN
27	37	56.9	804	1	VP5_WTV
28	37	56.9	1298	1	VGR3_HUMAN
29	36.5	56.2	355	1	AAR2_YEAST
30	36	55.4	209	1	COAT_TRVPS
31	36	55.4	243	1	YOEF_BACSU
32	36	55.4	260	1	TH14_ARCFU
33	36	55.4	316	1	YQ15_CABEL
					Q92978 caenorhabdi

34 36 55.4 447 1 HST3\_YEAST  
35 36 55.4 506 1 YF26\_SYNY3  
36 36 55.4 531 1 YQCG\_BACSU  
37 36 55.4 694 1 FRES\_YEAST  
38 36 55.4 724 1 CAO2\_CANMA  
39 36 55.4 897 1 BGAL\_CLOAB  
40 36 55.4 1094 1 YB00\_YEAST  
41 36 55.4 1355 1 SALM\_DROME  
42 36 55.4 1402 1 SALM\_DROVI  
43 35 53.8 126 1 YVQI\_BACSU  
44 35 53.8 263 1 TH14\_METJA  
45 35 53.8 306 1 LUXD\_PHOPO

P53687 saccharomyc  
P74360 synchocyst  
P45942 bacillus su  
Q08908 saccharomyc  
Q00468 candida mal  
P24131 clostridium  
P38114 saccharomyc  
P39770 drosophila  
P39806 drosophila  
Q32202 bacillus su  
Q58018 methanococc  
P41302 photobacter

#### ALIGNMENTS

RESULT 1  
GHR\_BOVIN  
ID GHR\_BOVIN STANDARD; PRT; 634 AA.  
AC P79108;1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, last sequence update)  
DT 15-MAR-2004 (Rel. 43, last annotation update)  
DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).  
DE GHR.  
GN Bos taurus (Bovine).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
OC NCBI\_TaxID=9913;  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GIR; TISSUE=Liver;  
RA Souza S.C., Wang X., Lobo R.B., Kopchick J.J.;  
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 1.  
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.  
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CC -----  
CC EMBL; X70041; CAA49635.1; -.  
CC HSSP; P10912; 1A22.  
CC InterPro; IPR002996; CR1A.  
CC InterPro; IPR003961; FN III.  
CC InterPro; IPR003528; Hemtopoptn\_L\_Fl.  
CC Pfam; PF00041; fn3; 1.  
CC SMART; SM00060; FN3; 1.  
CC PROSITE; PS01352; HEMATOPO REC L Fl; 1.  
CC Receptor; Transmembrane; Glycoprotein; signal.  
FT SIGNAL 1 18  
FT CHAIN 19 634  
FT DOMAIN 19 260  
FT TRANSMEM 261 284  
FT DOMAIN 285 634  
FT DOMAIN 141 248  
FT DISULFID 56 66  
FT DISULFID 97 108  
FT DISULFID 122 136  
FT CARBOHYD 46 46  
FT CARBOHYD 73 73  
FT CARBOHYD 111 111

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FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 634 AA; 70979 MW; 91955A28296CBD2E CRC64;

Query Match 100.0%; Score 65; DB 1; Length 634;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
Db 335 DDSWVEFIELDI 346

RESULT 2
GHR_SHEEP
ID GHR_SHEEP STANDARD; PRT; 634 AA.
AC Q28575;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
DE GHR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91099608; PubMed=1980117;
RA Adams T.E., Baker L., Fiddes R.J., Brandon M.R.;
RT "The sheep growth hormone receptor: molecular cloning and ontogeny of
RT mRNA expression in the liver.";
RL Mol. Cell. Endocrinol. 73:135-145(1990).
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormones.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC -!- SIMILARITY: Subfamily 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC -!- SIMILARITY:
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M82912; AAA73171.1; -.
DR PIR; S33339; S33339.
DR HSSP; P10912; IAXI.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 18
FT CHAIN 19 634
FT DOMAIN 19 260
FT TRANSMEM 261 284
FT DOMAIN 285 634
FT DOMAIN 141 248
FT DISULFID 56 66
FT DISULFID 97 108
FT DISULFID 122 136
FT CARBOHYD 46 46
FT CARBOHYD 73 73
N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 634 AA; 70844 MW; FFD28B9C23EC1496 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 634;
Best Local Similarity 100.0%; Pred. No. 0.00069;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
Db 335 DDSWVEFIELDI 346

RESULT 3
GHR_HUMAN
ID GHR_HUMAN STANDARD; PRT; 638 AA.
AC P10312;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
DE GHR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=88065896; PubMed=2825030;
RA Leung D.W., Spencer S.A., Cachianes G., Hammonds R.G., Collins C.,
RA Henzel W.J., Barnard R., Waters M.J., Wood W.I.;
RT "Growth hormone receptor and serum binding protein: purification,
RT cloning and expression.";
RL Nature 330:537-543(1987).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT LEU-544.
RX MEDLINE=90046742; PubMed=2813379;
RA Godowski P.J., Leung D.W., Meacham L.R., Galgani J.P., Hellmiss R.,
RA Keret R., Rotwein P.S., Parks J.S., Laron Z., Wood W.I.;
RT "Characterization of the human growth hormone receptor gene and
RT demonstration of a partial gene deletion in two patients with Laron-
RT type dwarfism.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8083-8087(1989).
RN [3]
RX DISULFIDE BONDS.
RX MEDLINE=90153957; PubMed=2406245;
RA Fuh G., Mulkerrin M.G., Bass S., McFarland N., Brochier M.,
RA Bourrel J.H., Light D.R., Wells J.A.;
RT "The human growth hormone receptor: Secretion from Escherichia coli
RT and disulfide bonding pattern of the extracellular binding domain.";
J. Biol. Chem. 265:3111-3115(1990).
RN [4]
RX VARIANT LARON DWARFISM SER-114.
RX MEDLINE=89384829; PubMed=2779634;
RA Amsellem S., Duquesnoy P., Attree O., Novelli G., Bousnina S.,
RA Postelvinay M.-C., Goossens M.;
RT "Laron dwarfism and mutations of the growth hormone-receptor gene.";
New Engl. J. Med. 321:989-995(1989).
RN [5]
RX VARIANTS LARON DWARFISM.
RX MEDLINE=93278381; PubMed=8504296;
RA Amsellem S., Duquesnoy P., Duriez B., Dastot F., Sorbier M.-L.,
RA Valleix S., Goossens M.;
RT "Spectrum of growth hormone receptor mutations and associated
RT haplotypes in Laron syndrome.";
Hum. Mol. Genet. 2:355-359(1993).
RN [6]
RX VARIANT LARON DWARFISM HIS-170.
RX MEDLINE=94185645; PubMed=8137822;

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Best Local Similarity 100.0%; Pred. No. 0.0007;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12  
Db 339 DDSWVEFIELDI 350

## RESULT 4

CHR_MACMU	STANDARD;	PRT;	638 AA.
ID	GHR_MACMU		
AC	P79194;		
DT	15-JUL-1998 (Rel. 36, Created)		
DT	15-JUL-1998 (Rel. 36, Last sequence update)		
DT	15-MAR-2004 (Rel. 43, Last annotation update)		
DE	Growth hormone receptor precursor (GH receptor) (Serum binding protein).		
DE	GHR.		
OS	Macaca mulatta (Rhesus macaque).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;		
OC	Cercopitheinae; Macaca.		
OX	NCBI_TaxID=9544;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97373601; PubMed=9228076;		
RA	Martini J.P., Pezet A., Guezennec C.Y., Edery M., Postel-Vinay M.C.,		
RA	Kelly P.A.;		
RT	"Monkey growth hormone (GH) receptor gene expression. Evidence for		
RT	two mechanisms for the generation of the GH binding protein.";		
RL	J. Biol. Chem. 272:18951-18958(1997).		
CC	!- FUNCTION: This is a receptor for pituitary gland growth hormone.		
CC	!- SUBUNIT: Homodimer (By similarity).		
CC	!- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	!- SIMILARITY: Belongs to the type I cytokine family of receptors.		
CC	Subfamily 1.		
CC	!- SIMILARITY: Contains 1 fibronectin type III domain.		

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CC	EMBL; U84589; AAB47702.1; --	
DR	HSP; P10912; 1AXI.	
DR	InterPro; IPR002996; CRIA.	
DR	InterPro; IPR003961; FN III.	
DR	InterPro; IPR003528; Hemtopoptn_L_F1.	
DR	SMART; SM00060; FN3; 1.	
DR	PROSITE; PS01352; HEMATOPO. REC L_F1; 1.	
KW	Receptor; Transmembrane; Glycoprotein; Signal.	
FT	SIGNAL	1..8
FT	CHAIN	19..638
FT	DOMAIN	19..254
FT	TRANSMEM	265..288
FT	DOMAIN	289..638
FT	DOMAIN	145..252
FT	DISULFID	56..66
FT	DISULFID	101..132
FT	DISULFID	126..140
FT	SEQUENCE	638 AA; 1F81A5301625F8E CRC64;
SQ		

```
Query Match      100.0%; Score 65; DB 1; Length 638;
Best Local Similarity 100.0%; Pred.No. 0.0007;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 DDSWVEFIELDI 12  
|||  
D6 339 DDSWVEFIELDI 350

## RESULT 6

## RESULT 5

```

GHR_PIG
ID GHR_PIG STANDARD; PRT; 638 AA.
AC AC
FT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-WAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
DE GHR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
SEQUENCE FROM N.A.
RN STRAIN=Landrace-Yorkshire; TISSUE=Liver;
RX MEDLINE=91057155; PubMed=2243805;
RC Cioffi J.A., Wang X., Kopchick J.J.;
RT "Porcine growth hormone receptor cDNA sequence.";
RL Nucleic Acids Res. 18:6451-6451(1990).
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC -!- Subfamily 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outsta
CC the European Bioinformatics Institute. There are no restrictions o
CC use by non-profit institutions as long as its content is in n
CC modified and this statement is not removed. Usage by and for commu
CC enties requires a license agreement (See http://www.isb-sib.ch/ann
CC or send an email to license@isb-sib.ch).
CC

```

CC  
-----  
EMBL; X54429; CAA38301.1; --  
DR DR  
FIR; S12136; S12136.  
DR DR  
HSSP; P10912; 1A22.  
DR DR  
TaterPro; IPR002996; CRIA.  
DR DR  
InterPro; IPR003961; FN.III.  
DR DR  
InterPro; IPR003528; Hemoptoptn\_L.Fl.  
DR DR  
Pfam; PF00041; fn3; 1.  
DR DR  
SMART; SM00060; FN3; 1.  
DR DR  
PROSITE; PS01352; HENATOPO REC L.Fl; 1.  
DR DR  
Receptor; Transmembrane; Glycoprotein; Signal.  
KW

FT	1	18	
SIGNAL			GROWTH HORMONE RECEPTOR.
FT	19	638	EXTRACELLULAR (POTENTIAL).
FT	284		POTENTIAL.
FT	285	288	CYTOSOLIC (POTENTIAL).
FT	289	638	FIBRONECTIN TYPE-III.
FT	145	252	BY SIMILARITY.
FT	56	66	BY SIMILARITY.
FT	101	112	BY SIMILARITY.
FT	DISULFID		BY SIMILARITY.
FT	DISULFID	126	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	46	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	115	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	156	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	161	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	200	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	200	N-LINKED (GLCNAC. .) (POTENTIAL).
SQ	SEQUENCE	638 AA; 71145	NW; BC7C66536FDFF97 CRC64;

```
Query Match      100.0%; Score 65; DB 1; Length 638;
Best Local Similarity 100.0%; Pred. No. 0.0007;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	DDSWVEFIELDI	12
Db	339	DDSWVEFIELDI	350

GHR\_RABIT STANDARD; PRT; 638 AA.

AC PI9941; (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).

DE protein).

GN GHR.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE=88065936; PubMed=2825030;

RA Leung D.W., Spencer S.A., Cachianes G., Hammonds R.G., Collins C., Hensel W.J., Barnard R., Waters M.J., Wood W.I.;

RT "Growth hormone receptor and serum binding protein: purification, cloning and expression.";

RL Nature 330:537-543(1987).

CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.

CC -!- SUBUNIT: Homodimer.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.

CC Subfamily 1.

CC -!- SIMILARITY: Contains 1 fibronectin type III domain.

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CC -----

DR EMBL; AF015252; AAB67613.1; -.

DR PIR; S08544; B28176.

DR HSP; P10912; I422.

DR InterPro; IPR002996; CR1A.

DR InterPro; IPR003961; FN III.

DR Pfam; PF00041; fn3; 1.

DR SMART; SM00060; FN3; 1.

DR PROSITE; PS01352; HEMATOPO REC L\_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 18

FT CHAIN 19 638 GROWTH HORMONE RECEPTOR.

FT DOMAIN 19 264 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 265 288 POTENTIAL.

FT DOMAIN 289 638 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 145 252 FIBRONECTIN TYPE-III.

FT DISULFID 56 66 BY SIMILARITY.

FT DISULFID 101 112 BY SIMILARITY.

FT DISULFID 126 140 BY SIMILARITY.

FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 638 AA; 71076 MW; E05CCED1D7294624C CRC64;

Query Match 100.0%; Score 65; DB 1; Length 638;

Best Local Similarity 100.0%; Pred. No. 0.0007;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12

Db 339 DDSWVEFIELDI 350

RESULT 7  
GHR\_RAT

GHR\_RAT STANDARD; PRT; 638 AA.

AC PI6310; (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).

DE protein).

GN GHR.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=101116;

RN [1] SEQUENCE FROM N.A.

RX MEDLINE=89255563; PubMed=2722883;

RA Mathews L.S., Emberg B., Norstedt G.;

RT "Regulation of rat growth hormone receptor gene expression.";

RL J. Biol. Chem. 264:9905-9910(1989).

RN [2] SEQUENCE FROM N.A.

RP MEDLINE=90006741; PubMed=2792761;

RX Baumbach W.R., Horner D.L., Logan J.S.;

RA "The growth hormone-binding protein in rat serum is an alternatively spliced form of the rat growth hormone receptor.";

RT Genes Dev. 3:1199-1205(1989).

RL Genes Dev. 3:1199-1205(1989).

CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.

CC -!- SUBUNIT: Homodimer.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.

CC Subfamily 1.

CC -!- SIMILARITY: Contains 1 fibronectin type III domain.

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CC -----

DR EMBL; J04811; AAA41219.1; -.

DR PIR; A32985; A33505.

DR HSP; P10912; I422.

DR InterPro; IPR002996; CR1A.

DR InterPro; IPR003961; FN III.

DR InterPro; IPR003528; Hemtopoptn\_L\_F1.

DR Pfam; PF00041; fn3; 1.

DR SMART; SM00060; FN3; 1.

DR PROSITE; PS01352; HEMATOPO REC L\_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 18

FT CHAIN 19 638 GROWTH HORMONE RECEPTOR.

FT DOMAIN 19 265 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 266 289 POTENTIAL.

FT DOMAIN 290 638 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 145 252 FIBRONECTIN TYPE-III.

FT DISULFID 56 66 BY SIMILARITY.

FT DISULFID 101 112 BY SIMILARITY.

FT DISULFID 126 140 BY SIMILARITY.

FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 638 AA; 71236 MW; 0D8E9AF759A21A3B CRC64;

Query Match 100.0%; Score 65; DB 1; Length 638;

Best Local Similarity 100.0%; Pred. No. 0.0007;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12

Db 340 DDSWVEFIELDI 351

```
RESULT 8
GHR_MOUSE
ID GHR_MOUSE STANDARD; PRT; 650 AA.
AC P16882; P16590; Q9R264;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GHR receptor) (GHR binding protein)
DE (GHBP) (Serum binding protein).
GN GHR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=89295449; PubMed=2739661;
RA Smith W.C., Kuniyoshi J., Talamantes F.;
RT "Mouse serum growth hormone (GH) binding protein has GH receptor
RT extracellular and substituted transmembrane domains.";
RL Mol. Endocrinol. 3:984-990(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=9367316; PubMed=10425445;
RA Moffat J.G., Edens A., Talamantes F.;
RT "Structure and expression of the mouse growth hormone receptor/growth
RT hormone binding protein gene.";
RL J. Mol. Endocrinol. 23:33-44(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=95080157; PubMed=7988474;
RA Edens A., Southard J.N., Talamantes F.;
RT "Mouse growth hormone receptor/binding protein and growth hormone
RT receptor transcripts are produced from a single gene by alternative
RT splicing.";
RL Endocrinology 135:2802-2805(1994).
RN [4]
RP SEQUENCE OF 156-650 FROM N.A. (ISOFORM 1).
RX STRAIN=C57BL/6;
RA Zhou Y., He L., Knochick J.J.;
RT "An exon encoding the mouse growth hormone binding protein (mGHBP)
RT carboxy terminus is located between exon 7 and 8 of the mouse growth
RT hormone receptor gene.";
RL Receptor 4:223-227(1994).
RN [5]
RP REVISIONS.
RA Zhou Y., He L., Knochick J.J.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 25-41.
RX MEDLINE=88288223; PubMed=3398846;
RA Smith W.C., Colosi P., Talamantes F.;
RT "Isolation of two molecular weight variants of the mouse growth
RT hormone receptor.";
RL Mol. Endocrinol. 2:108-116(1988).
RN [7]
RP -1- FUNCTION: Isoform 1 is a receptor for pituitary gland growth
CC hormone. Isoform 2 is a serum growth hormone binding protein that
CC may play an important role in regulating the effective serum
CC concentration of gh.
CC
CC -1- SUBUNIT: Isoform 1 is a homodimer.
CC
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC Secreted (isoform 2).
CC
CC -1- ALTERNATIVE PRODUCTS:
CC Name=1; Synonyms=HWM GHR;
CC IsoId=P16882-1; Sequence=Displayed;
CC Name=2; Synonyms=LWM GHR;
CC IsoId=P16882-2; Sequence=VSP_001716, VSP_001717;
CC
CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC
```

Subfamily 1.

-1- SIMILARITY: Contains 1 fibronectin type III domain.

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EMBL; M33324; AAA37690.1; ALT SEQ.  
EMBL; M31680; AAA37689.1; ALT\_SEQ.  
EMBL; AF120489; AAD32556.1; -  
EMBL; AF120481; AAD32556.1; JOINED.  
EMBL; AF120482; AAD32556.1; JOINED.  
EMBL; AF120483; AAD32556.1; JOINED.  
EMBL; AF120484; AAD32556.1; JOINED.  
EMBL; AF120485; AAD32556.1; JOINED.  
EMBL; AF120486; AAD32556.1; JOINED.  
EMBL; AF120487; AAD32556.1; JOINED.  
EMBL; AF120488; AAD32556.1; JOINED.  
EMBL; AF120487; AAD32555.1; -  
EMBL; AF120481; AAD32555.1; JOINED.  
EMBL; AF120482; AAD32555.1; JOINED.  
EMBL; AF120483; AAD32555.1; JOINED.  
EMBL; AF120484; AAD32555.1; JOINED.  
EMBL; AF120485; AAD32555.1; JOINED.  
EMBL; AF120486; AAD32555.1; JOINED.  
EMBL; U49266; AAK62802.1; -  
EMBL; U49268; AAK62802.1; JOINED.  
EMBL; U43933; AAK62802.1; JOINED.  
HSP; P10912; I422.  
MGD; MGI:95708; Chr.  
InterPro; IPR002996; CRLA.  
InterPro; IPR003961; FN III.  
InterPro; IPR003528; Hemtopoptn\_L\_F1.  
SMART; SM00060; FN3.1.  
PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.

FT	SIGNAL	1	24
FT	CHAIN	25	650
FT	DOMAIN	25	273
FT	TRANSMEM	274	297
FT	DOMAIN	298	650
FT	DOMAIN	153	260
FT	DISULFID	56	66
FT	DISULFID	109	120
FT	DISULFID	134	148
FT	CARBOHYD	123	123
FT	CARBOHYD	164	164
FT	CARBOHYD	169	169
FT	CARBOHYD	208	208
FT	VARSPPLIC	271	296
FT	VARSPPLIC	297	650
FT	CONFLICT	25	25
FT	CONFLICT	162	162
FT	CONFLICT	325	325
FT	CONFLICT	423	423
FT	SEQUENCE	650 AA;	72783 MW; 95653380CAFOB931 CRC64;

Query Match 100.0%; Score 65; DB 1; Length 650;  
Best Local Similarity 100.0%; Pred. No. 0.00071;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	DDSWVRFELDI	12
Db	348	DDSWVRFELDI	359

```

RESULT 9
GHR CHICK
ID GHR CHICK STANDARD; PRT; 608 AA.
AC Q02092;
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
DE GHR.
GN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91243665; PubMed=2036984;
RA Burnside J., Liou S.S., Cogburn L.A.;
RT "Molecular cloning of the chicken growth hormone receptor
RT complementary deoxyribonucleic acid: mutation of the gene in
RT sex-linked dwarf chickens."
RL Endocrinology 128:3183-3192(1991).
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Broad specificity.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M74057; AAA48781.1; -.
CC PIR; S32823; S32823.
CC HSSP; P10912; IAXI.
CC InterPro; IPR002996; CRIA.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR003528; Hemtopoptn_L_F1.
CC Pfam; PF00041; fn3; 1.
CC SMART; SM00060; FN3; 1.
CC PROSITE; PS01352; HEMATOPO REC L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 16
FT CHAIN 17 608 GROWTH HORMONE RECEPTOR.
FT DOMAIN 17 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 261 POTENTIAL.
FT DOMAIN 262 608 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 117 223 FIBRONECTIN TYPE-III.
FT DISULFID 34 44 BY SIMILARITY.
FT DISULFID 72 83 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 608 AA; 68572 MW; D71AD7B6C62528DC CRC64;

Query Match 90.8%; Score 59; DB 1; Length 608;
Best Local Similarity 91.7%; Pred. No. 0.0078;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
Db 312 DDLWVEFIELDI 323

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RESULT 10
GHR COLLI
ID GHR COLLI STANDARD; PRT; 611 AA.
AC Q90375;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
DE GHR.
GN Columba livia (Domestic pigeon).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columbae;
OX NCBI_TaxID=8932;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Cheng C.H.K., Shaw P.C., Tsai K.W.K., Lau K.F.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC -!- SIMILARITY: Subfamily 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U20353; AAA84745.1; -.
CC HSSP; P10912; IAXI.
CC InterPro; IPR002996; CRIA.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR003528; Hemtopoptn_L_F1.
CC Pfam; PF00041; fn3; 1.
CC SMART; SM00060; FN3; 1.
CC PROSITE; PS01352; HEMATOPO REC L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 611 GROWTH HORMONE RECEPTOR.
FT DOMAIN 21 240 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 241 264 POTENTIAL.
FT DOMAIN 265 611 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 119 226 FIBRONECTIN TYPE-III.
FT DISULFID 34 44 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT DISULFID 100 114 BY SIMILARITY.
FT CARBOHYD 16 16 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 89 89 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 130 130 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 611 AA; 68851 MW; C48750BF9EB4EBDA CRC64;

Query Match 90.8%; Score 59; DB 1; Length 611;
Best Local Similarity 91.7%; Pred. No. 0.0078;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
Db 315 DDLWVEFIELDI 326

```

RESULT 11

RPOC\_PSEPU STANDARD; PRT; 1409 AA.  
 AC RPOC\_PSEPU  
 DT 01-NOV-1990 (Rel. 15, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE DNA-directed RNA polymerase beta' chain (EC 2.7.6) (Transcriptase  
 DE beta' chain) (RNA polymerase beta' subunit).  
 OS Pseudomonas putida.  
 GN Pseudomonas putida.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=303;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Danilovich A.V., Borodin A.M., Allikmets R.L., Rostapshov V.M.,  
 RA Chernov I.P., Azhikina T.L., Monastyrskaya G.S., Sverdlov E.D.;  
 RT "Nucleotide sequence of the rpoC gene coding for the beta'-subunit of  
 RT RNA polymerase in Pseudomonas putida.";  
 RL Dokl. Biochem. 303:241-245(1998).  
 RN [2]  
 RN SEQUENCE OF 1-497 FROM N.A.  
 RP MEDLINE=89117617; PubMed=3219133;  
 RX Borodin A.M., Danilovich A.V., Chernov I.P., Azhikina T.L.,  
 RA Rostapshov V.M., Monastyrskaya G.S.;  
 RT "Genes coding for RNA polymerase in bacteria. III. The use of  
 RT modified Sanger's method for sequencing the C-terminal region of rpoB  
 RT gene, N-terminal region of rpoC gene and intercistron region of RNA  
 RT polymerase in Pseudomonas putida.";  
 RL Bioorg. Khim. 14:1179-1182(1988).  
 CC -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription  
 CC of DNA into RNA using the four ribonucleoside triphosphates as  
 CC substrates.  
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
 CC [RNA](N).  
 CC -1- SUBUNIT: The enzyme consists of the sigma chain and the core  
 CC enzyme which is composed of 2 alpha chains, 1 beta chain, and 1  
 CC beta' chain.  
 CC -1- SIMILARITY: Belongs to the RNA polymerase beta' chain family.  
 CC  
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 CC  
 CC EMBL; X16538; CAA34538.1; --  
 CC EMBL; M38319; AAA25987.1; --  
 CC PIR; JN0420; JN0420.  
 CC HSSP; Q9KWU6; 1HQM.  
 CC InterPro; IPR000722; RNA\_pol\_A.  
 CC InterPro; IPR007080; RNA\_pol\_Rpb1\_1.  
 CC InterPro; IPR007066; RNA\_pol\_Rpb1\_3.  
 CC InterPro; IPR007083; RNA\_pol\_Rpb1\_4.  
 CC InterPro; IPR007081; RNA\_pol\_Rpb1\_5.  
 CC InterPro; IPR006592; RNA\_pol\_N.  
 CC Pfam; PF04997; RNA\_pol\_Rpb1\_1; 1.  
 CC Pfam; PF00623; RNA\_pol\_Rpb1\_2; 1.  
 CC Pfam; PF04983; RNA\_pol\_Rpb1\_3; 1.  
 CC Pfam; PF05000; RNA\_pol\_Rpb1\_4; 1.  
 CC Pfam; PF04998; RNA\_pol\_Rpb1\_5; 1.  
 CC SMART; SM00663; RPOLA\_N; 1.  
 KW Transference; DNA-directed RNA polymerase; Transcription.  
 FT CONFLICT 2 2 P -> L (IN REF. 2).  
 FT CONFLICT 17 17 N -> I (IN REF. 2).  
 FT CONFLICT 89 89 L -> V (IN REF. 2).  
 FT CONFLICT 203 203 I -> T (IN REF. 2).  
 FT CONFLICT 328 328 I -> T (IN REF. 2).  
 FT CONFLICT 335 335 L -> S (IN REF. 2).  
 FT CONFLICT 348 348 L -> R (IN REF. 2).  
 FT CONFLICT 482 482 P -> L (IN REF. 2).  
 FT CONFLICT 482 482

FT CONFLICT 484 484 T -> I (IN REF. 2).  
 SQ SEQUENCE 1409 AA; 154544 MW; C5662109D3B3D81 CRC64;  
 Query Match 73.8%; Score 48; DB 1; Length 1409;  
 Best Local Similarity 72.7%; Pred. No. 1.8;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 DDSWVERIELD 11  
 Db 876 DEQWVEFIEN 886  
 RESULT 12  
 SSP2\_BOMMO STANDARD; PRT; 704 AA.  
 ID SSP2\_BOMMO  
 AC P20613;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Sex-specific storage-protein 2 precursor.  
 GN SP2.  
 OS Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
 OC Bombycidae; Bombyx.  
 OX NCBI\_TaxID=7091;  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89291839; PubMed=2544581;  
 RA Fujii T., Sakurai H., Izumi S., Tomino S.;  
 RT "Structure of the gene for the arylphorin-type storage protein SP 2  
 RT of Bombyx mori.";  
 RL J. Biol. Chem. 264:11020-11025(1989).  
 CC -1- FUNCTION: Larval storage protein (LSP) which may serve as a store  
 CC of amino acids for synthesis of adult proteins.  
 CC -1- SUBCELLULAR LOCATION: Extracellular.  
 CC -1- TISSUE SPECIFICITY: Fat body.  
 CC -1- SIMILARITY: TO ARYLPHORINS AND TO ARTHROPOD HEMOCYANINS.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M24370; AAA27848.1; --  
 CC EMBL; M24371; AAA27848.1; JOINED.  
 CC PIR; A34287; A34287.  
 CC HSSP; P04253; 1QXY.  
 CC InterPro; IPR008922; Di-copper\_centre.  
 CC InterPro; IPR000896; Hemocyanin.  
 CC InterPro; IPR005203; Hemocyanin\_C.  
 CC InterPro; IPR005204; Hemocyanin\_N.  
 CC InterPro; IPR007110; Ig-like.  
 CC Pfam; PF00372; hemocyanin; 1.  
 CC Pfam; PF03723; hemocyanin\_C; 1.  
 CC Pfam; PF03722; hemocyanin\_N; 1.  
 CC PRINTS; PR00187; HAEMOCYANIN.  
 CC PROSITE; PS00209; HAEMOCYANIN.  
 CC PROSITE; PS00210; HAEMOCYANIN\_1; 1.  
 CC PROSITE; PS00210; HAEMOCYANIN\_2; 1.  
 KW Signal; Storage protein; Glycoprotein.  
 FT SIGNAL 1 16  
 FT CHAIN 17 704 SEX-SPECIFIC STORAGE-PROTEIN 2.  
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 681 681 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 704 AA; 83466 MW; 365E7DFE707137EB CRC64;  
 Query Match 66.2%; Score 43; DB 1; Length 704;  
 Best Local Similarity 54.5%; Pred. No. 6.6;

Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 DDSWVERFIELD 11  
Db 543 EDNMKFFELD 553

## RESULT 13

Y4FP\_RHISN STANDARD; PRT; 358 AA.  
ID AC P55454;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Probable ABC transporter periplasmic binding protein Y4FP precursor.  
GN Y4FP.  
OS Rhizobium sp. (strain NGR234).  
OG Plasmid sym pNGR234a.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.  
OX NCBI\_TaxID=394;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97305956; PubMed=9163424;  
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,  
RA Perret X.  
RT "Molecular basis of symbiosis between Rhizobium and legumes."  
RL Nature 387:394-401(1997).  
CC -1- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT  
CC SYSTEM Y4FPNP.  
CC -1- SUBCELLULAR LOCATION: Periplasmic (Potential).  
CC -1- SIMILARITY: SOME, TO S.MARCESCENS IRON(III)-BINDING PERIPLASMIC  
CC PROTEIN AND TO H.INFLUENZAE HI0131.  
CC -1- CAUTION: It is uncertain whether Met-1 is the initiator.

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EMBL: AE000073; AAB91672.1; -;  
DR InterPro; IPR006059; SBP\_bac\_1.  
DR Pfam; PF01547; SBP\_bac\_1; 1.  
KW Hypothetical protein; Transport; Periplasmic; Signal; Plasmid.  
FT SIGNAL 1 46 OR 34, OR 40, OR 41 (POTENTIAL).  
FT CHAIN 47 358 PROBABLE ABC TRANSPORTER PERIPLASMIC  
FT BINDING PROTEIN Y4FP.  
SQ SEQUENCE 358 AA; 39015 MW; B485BC3FA3B4D229 CRC64;

Query Match 61.5%; Score 40; DB 1; Length 358;  
Best Local Similarity 63.6%; Pred. No. 11;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DDSWVERFIELDI 12  
Db 346 DSWLQKIELEI 356

## RESULT 14

VGR3\_MOUSE STANDARD; PRT; 1363 AA.  
ID AC P35917;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Vascular endothelial growth factor receptor 3 precursor (EC 2.7.1.112)  
DE (VEGFR-3) (tyrosine-protein kinase receptor FLT4).  
GN FLT4 OR FLT-4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/6J;  
RX MEDLINE=93330572; PubMed=8393164;  
RA Finnerty H., Kelleher K., Morris G.E., Bean K., Merberg D.M.,  
RA Kriz R., Morris J.C., Sookdeo H., Turner K.J., Wood C.R.;  
RT "Molecular cloning of murine FLT and FLT4."  
RL Oncogene 8:2293-2298(1993).  
CC -1- FUNCTION: RECEPTOR FOR VEGF-C. HAS A TYROSINE-PROTEIN KINASE  
CC ACTIVITY.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC FETAL LIVER, BRAIN, INTESTINE AND PLACENTA.  
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases.  
CC CSF-1/PDGF receptor subfamily.  
CC -1- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.  
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EMBL: L07296; AAA40077.1; -;  
DR PIR; I58375; I58375.  
DR HSP; P11362; IFGK.  
DR MGD; MGI:95561; Flt4.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR001824; RecepttyrkinIII.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR InterPro; IPR008266; Tyr\_kinase\_AS.  
DR Pfam; PF00047; Ig; 5.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 2.  
DR SMART; SM00408; IGC2; 2.  
DR SMART; SM00219; TyKc; 1.  
DR PROSITE; PS00835; IG\_LIKE; 5.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00109; PROTEIN KINASE TVR; 1.  
DR PROSITE; PS00240; RECEPTOR\_TYR\_KIN\_III; 1.  
KW Transferase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;  
KW Receptor; Transmembrane; Signal; Immunoglobulin domain; Repeat;  
KW Glycoprotein.  
FT SIGNAL 1 24 POTENTIAL.  
FT CHAIN 25 1363 VASCULAR ENDOTHELIAL GROWTH FACTOR  
FT RECEPTOR 3.  
FT DOMAIN 25 775 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 776 797 POTENTIAL.  
FT DOMAIN 798 1363 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 44 118 IG-LIKE C2-TYPE 1.  
FT DOMAIN 151 213 IG-LIKE C2-TYPE 2.  
FT DOMAIN 230 326 IG-LIKE C2-TYPE 3.  
FT DOMAIN 331 415 IG-LIKE C2-TYPE 4.  
FT DOMAIN 422 552 IG-LIKE C2-TYPE 5.  
FT DOMAIN 555 671 IG-LIKE C2-TYPE 6.  
FT DOMAIN 678 764 IG-LIKE C2-TYPE 7.  
FT DOMAIN 845 1173 PROTEIN KINASE.  
FT NP\_BIND 851 859 ATP (BY SIMILARITY).  
FT BINDING 879 879 ATP (BY SIMILARITY).  
FT ACT\_SITE 1037 1037 BY SIMILARITY.  
FT DISULFID 51 111 POTENTIAL.  
FT DISULFID 158 206 POTENTIAL.  
FT DISULFID 252 310 POTENTIAL.

```
FT DISULFID 445 534 POTENTIAL.
FT DISULFID 578 653 POTENTIAL.
FT DISULFID 699 751 POTENTIAL.
FT MOD RES 1068 1068 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 527 527 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 582 582 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 594 594 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 683 683 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 690 690 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 758 758 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1363 AA; 153015 MW; F1BF8A2BDEF99BE9 CRC64;

Query Match 61.5%; Score 40; DB 1; Length 1363;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DSWVEFIE 9
Db 505 DSWTEFVE 512

RESULT 15
SR09_MAIZE
ID -SR09_MAIZE STANDARD; PRT; 103 AA.
AC 004438;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Signal recognition particie 9 kDa protein (SRP9).
GN SRP9.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. W64A2;
RA Bui N., Wolff N., Strub K.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Signal-recognition-particle assembly has a crucial role
CC in targeting secretory proteins to the rough endoplasmic reticulum
CC membrane. SRP9 together with SRP14 and the Alu portion of the SRP
CC RNA, constitutes the elongation arrest domain of SRP. The complex
CC of SRP9 and SRP14 is required for SRP RNA binding (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the SRP9 family.
CC -----
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CC -----
CC EMBL; Y10117; CAA71203.1; -.
CC PIR; T03951; T03951.
CC HSPP; P49962; 1914.
CC InterPro; IPR008832; SRP9.
CC InterPro; IPR009018; SRP9/14.
CC Pfam; PF05486; SRP9; 1.
CC Signal recognition particie; RNA-binding.
SQ SEQUENCE 103 AA; 12077 MW; B6EFA49DA77C13BE CRC64;

Query Match 60.0%; Score 39; DB 1; Length 103;
```

```
Best Local Similarity 54.5%; Pred. No. 4.2;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DSWVEFIELDI 12
Db 5 DSWEEFVERSV 15

Search completed: June 9, 2004, 15:49:05
Job time : 9.75676 secs
```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 9, 2004, 15:43:00 ; Search time 40.2162 Seconds

(without alignments)  
94.147 Million cell updates/sec

Title: US-09-660-302D-2

Perfect score: 65

Sequence: 1 DDSWVEFIELDI 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	100.0	101	6	Q863N9
2	65	100.0	105	6	Q863Q6
3	65	100.0	105	6	Q863P4
4	65	100.0	106	6	Q863Q3
5	65	100.0	106	6	Q863Q2
6	65	100.0	107	6	Q863Q9
7	65	100.0	107	6	Q863Q8
8	65	100.0	107	6	Q863Q7
9	65	100.0	107	6	Q863Q5
10	65	100.0	107	6	Q863Q4
11	65	100.0	107	6	Q863Q1
12	65	100.0	107	6	Q863Q0
13	65	100.0	107	6	Q863P9
14	65	100.0	107	6	Q863P8
15	65	100.0	107	6	Q863P7
16	65	100.0	107	6	Q863P6

17	65	100.0	107	6	Q863P5
18	65	100.0	107	6	Q863P2
19	65	100.0	107	6	Q863P1
20	65	100.0	107	6	Q863P0
21	65	100.0	107	6	Q863N8
22	65	100.0	107	6	Q863N7
23	65	100.0	107	6	Q863N6
24	65	100.0	130	11	Q99MY7
25	65	100.0	233	6	Q95MM1
26	65	100.0	238	11	Q924F8
27	65	100.0	293	6	Q8MJM2
28	65	100.0	294	6	Q95ML9
29	65	100.0	294	6	Q8MJL9
30	65	100.0	295	6	Q95ML8
31	65	100.0	295	11	Q80Z48
32	65	100.0	296	11	Q924F4
33	65	100.0	296	11	Q924F1
34	65	100.0	296	11	Q924E8
35	65	100.0	296	11	Q924F2
36	65	100.0	296	11	Q924E9
37	65	100.0	296	11	Q924F0
38	65	100.0	296	11	Q80Z55
39	65	100.0	296	11	Q80Z54
40	65	100.0	296	11	Q80Z53
41	65	100.0	296	11	Q80Z52
42	65	100.0	296	11	Q80Z51
43	65	100.0	296	11	Q80Z49
44	65	100.0	296	11	Q80Z47
45	65	100.0	296	11	Q80Z46

#### ALIGNMENTS

#### RESULT 1

ID Q863N9 PRELIMINARY; PRT; 101 AA.  
AC Q863N9, 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Growth hormone receptor (Fragment).  
GN GHR.  
OS Actonyx collaris.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae;  
OC Actonyx.  
CX NCBI\_TaxID=139309;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Keopfli K.-P., Wayne R.K.;  
RT "Type-1 SIS Markers Are More Informative Than Cytochrome b in  
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";  
RL Syst. Biol. 0:0-0(2003).  
DR EMBL; AF498204; AAP19695.1; -;  
DR GO; GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
FT NON\_TER 1 1  
FT NON\_TER 101 101  
SQ SEQUENCE 101 AA; 11428 MW; AD696CB6E0EBD7AC CRC64;

Query Match 100.0%; Score 65; DB 6; Length 101;  
Best Local Similarity 100.0%; Pred. No. 0.00054;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DDSWVEFIELDI 12

Db 24 DDSWVEFIELDI 35

#### RESULT 2

Q863Q6 PRELIMINARY; PRT; 105 AA.  
ID Q863Q6

```

AC Q863Q6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lontra canadensis (River otter) (Lutra canadensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Lontra.
OX NCBI_TaxID=76717;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498187; AAP19678.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 105
SQ SEQUENCE 105 AA; 11852 MW; F07A7052451EB8E7 CRC64;

Query Match 100.0%; Score 65; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12
Db 28 DDSWVEFIELDI 39

RESULT 3
Q863P4
ID Q863P4 PRELIMINARY; PRT; 105 AA.
AC Q863P4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Eira barbara (Tayra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Eira.
OX NCBI_TaxID=204263;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498199; AAP19690.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 105
SQ SEQUENCE 105 AA; 11879 MW; F6F6445250DB79BF CRC64;

Query Match 100.0%; Score 65; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.00056;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12
Db 28 DDSWVEFIELDI 39

RESULT 4
Q863Q3
ID Q863Q3 PRELIMINARY; PRT; 106 AA.
AC Q863Q3;

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DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lutra lutra (European river otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Lutra.
OX NCBI_TaxID=9657;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498130; AAP19681.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 106
SQ SEQUENCE 106 AA; 12006 MW; EFB0C6D8793AE9FF CRC64;

Query Match 100.0%; Score 65; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12
Db 29 DDSWVEFIELDI 40

RESULT 5
Q863Q2
ID Q863Q2 PRELIMINARY; PRT; 106 AA.
AC Q863Q2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lutra maculicollis (spotted necked otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Lutra.
OX NCBI_TaxID=76719;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498191; AAP19682.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 106
SQ SEQUENCE 106 AA; 12003 MW; EFB0DDAE24C29FF CRC64;

Query Match 100.0%; Score 65; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDSWVEFIELDI 12
Db 29 DDSWVEFIELDI 40

RESULT 6
Q863Q9
ID Q863Q9 PRELIMINARY; PRT; 107 AA.
AC Q863Q9;
DT 01-JUN-2003 (TREMBlrel. 24, Created)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Anonyx capensis (Cape clawless otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Anonyx.
OX NCBI_TaxID=76722;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498184; AAPI9675.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12101 MW; 7F3D579D3C26011B CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
Db 30 DDSWVEFIELDI 41

RESULT 7
Q863Q8 ID Q863Q8 PRELIMINARY; PRT; 107 AA.
AC Q863Q8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Amblyonyx cinereus (Asian small-clawed otter) (Anonyx cinereus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Amblyonyx.
OX NCBI_TaxID=55043;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498185; AAPI9676.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12121 MW; 84DD579D3C2EB8BA CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
Db 30 DDSWVEFIELDI 41

RESULT 8
Q863Q7 ID Q863Q7 PRELIMINARY; PRT; 107 AA.
AC Q863Q7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Enhydra lutris (Sea otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Enhydra.
OX NCBI_TaxID=34882;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498186; AAPI9677.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12151 MW; 84DD579D3C2EA9FE CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
Db 30 DDSWVEFIELDI 41

RESULT 9
Q863Q5 ID Q863Q5 PRELIMINARY; PRT; 107 AA.
AC Q863Q5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lontra felina (Sea cat) (Lutra felina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Lontra.
OX NCBI_TaxID=76718;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498188; AAPI9679.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12180 MW; 9113E140F3C5C3BB CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
Db 30 DDSWVEFIELDI 41

RESULT 10
Q863Q4 ID Q863Q4 PRELIMINARY; PRT; 107 AA.
AC Q863Q4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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DE Growth hormone receptor (Fragment).
GN GHR.
OS Lontra longicaudis (Neotropical otter) (Lutra longicaudis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Lontra.
OX NCBI_TaxID=71113;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498189; AAP19680.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12166 MW; 9113E146451EA8BB CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
   |||||
Db 30 DDSWVEFIELDI 41

RESULT 11
Q86301
ID Q863Q1 PRELIMINARY; PRT; 107 AA.
AC Q863Q1;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Pteronura brasiliensis (Giant otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Pteronura.
OX NCBI_TaxID=9672;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498192; AAP19683.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12137 MW; 96DBCA309E7789FE CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
   |||||
Db 30 DDSWVEFIELDI 41

RESULT 12
Q86300
ID Q863Q0 PRELIMINARY; PRT; 107 AA.
AC Q863Q0;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.

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GN GHR.
OS Mustela erminea (Ermine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=36723;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498193; AAP19684.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12140 MW; 96DBD146450149FE CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
   |||||
Db 30 DDSWVEFIELDI 41

RESULT 13
Q863P9
ID Q863P9 PRELIMINARY; PRT; 107 AA.
AC Q863P9;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Mustela frenata (Long-tailed weasel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=55048;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498194; AAP19685.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12140 MW; 96DBD146450149FE CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.00057;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12
   |||||
Db 30 DDSWVEFIELDI 41

RESULT 14
Q863P8
ID Q863P8 PRELIMINARY; PRT; 107 AA.
AC Q863P8;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.

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OS Mustela vison (American mink).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;  
 OC Mustela.  
 OX NCBI\_TaxID=9667;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Koepfli K.-P., Wayne R.K.;  
 RT "Type-1 STS Markers Are More Informative Than Cytochrome b in  
 RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";  
 RL Syst. Biol. 0:0-0(2003).  
 DR EMBL; AF498195; AAP19686.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 107  
 SQ SEQUENCE 107 AA; 12149 MW; 96CCE146450149FE CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.00057;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12  
 |||||  
 Db 30 DDSWVEFIELDI 41

RESULT 15  
 Q863P7  
 ID Q863P7 PRELIMINARY; PRT; 107 AA.  
 AC Q863P7;  
 DT 01-JUN-2003 (TReMBLrel. 24, Created)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE Growth hormone receptor (Fragment).  
 GN GHR.  
 OS Martes americana (American marten).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;  
 OC Martes.  
 OX NCBI\_TaxID=9660;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Koepfli K.-P., Wayne R.K.;  
 RT "Type-1 STS Markers Are More Informative Than Cytochrome b in  
 RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";  
 RL Syst. Biol. 0:0-0(2003).  
 DR EMBL; AF498196; AAP19687.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 107  
 SQ SEQUENCE 107 AA; 12172 MW; 96DBD14658B649FE CRC64;

Query Match 100.0%; Score 65; DB 6; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.00057;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DDSWVEFIELDI 12  
 |||||  
 Db 30 DDSWVEFIELDI 41

Search completed: June 9, 2004, 15:51:22  
 Job time : 40.2162 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2004, 15:36:10 ; Search time 50 seconds  
(without alignments)  
56.510 Million cell updates/sec

Title: US-09-660-302D-3  
Perfect score: 55  
Sequence: 1 DSWVEFIELD 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1596107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1596107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_29Jan04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	12	2 AAY32789	Aay32789 Growth ho
2	55	100.0	130	2 AAY32792	Aay32792 Growth ho
3	55	100.0	637	1 AAP92108	Aap92108 Human gro
4	55	100.0	638	1 AAP81326	Aap81326 Human gro
5	55	100.0	638	1 AAP81327	Aap81327 Rabbit gr
6	55	100.0	638	1 AAP92107	Aap92107 Rabbit gr
7	55	100.0	638	2 AAW33394	Aaw33394 Human gro
8	55	100.0	638	2 AAW33395	Aaw33395 Rabbit gr
9	55	100.0	638	7 ADD45061	Add45061 Rat Prote
10	55	100.0	638	7 ADD45067	Add45067 Human pro
11	55	100.0	638	7 ADD45063	Add45063 Human pro
12	55	100.0	638	7 ADD45065	Add45065 Rat Prote
13	55	100.0	648	4 ABB11437	Abb11437 Human gro
14	51	92.7	638	2 AAR06473	Aar06473 Serum som
15	49	89.1	12	2 AAY32793	Aay32793 Growth ho
16	49	89.1	12	2 AAY32794	Aay32794 Chicken g
17	49	89.1	608	2 AAR25246	Aar25246 Chicken g
18	43	78.2	705	5 ABB77350	Abb77350 Plodia in
19	42	76.4	1399	6 ABU41685	Abu41685 Protein e
20	42	76.4	1409	6 ABU39890	Abu39890 Protein e
21	40	72.7	1363	4 AAB37607	Aab37607 Human pro
22	40	72.7	1363	6 ABU04285	Abu04285 Human exp
23	39	70.9	14	6 ADA09064	Ada09064 Lanthanid
24	39	70.9	163	2 AAW20448	Aaw20448 H. pylori
25	39	70.9	255	3 AAB53166	Aab53166 Macaca mu

## ALIGNMENTS

RESULT 1  
AAY32789

ID AAY32789 standard; peptide; 12 AA.

XX AC AAY32789;

DT 09-NOV-1999 (first entry)

DE Growth hormone receptor polypeptide for inhibition of receptor cleavage.

KW Growth hormone receptor; signal transduction; proteolytic cleavage;

KW ubiquitin; proteosome binding site; muscle wasting; renal tubular defect;

KW uraemia; diabetes; Cushing's disease; eating disorder; AIDS.

XX OS Mammalia.

PN EP943624-AL.

PD 22-SEP-1999.

PF 12-MAR-1998; 98EP-00200799.

PR 12-MAR-1998; 98EP-00200799.

XX (UYUT-) RIJKSUNIV UTRECHT.

DR WPI; 1999-510566/43.

PT Controlling the availability and/or signal transduction capability of a cell surface receptor, useful for treating growth hormone deficiencies.

PS Claim 11; Page 27; 36pp; English.

XX This sequence is from the intracellular domain of the growth hormone receptor. This sequence is an example of a binding site motif AAY32790. This motif is used in a method for controlling the availability and signal transduction capability of a cell surface receptor by administering an inhibitor that is capable of inhibiting proteolytic cleavage of the receptor. Inhibition of this proteolytic cleavage results in the receptors being present on the surface for longer and therefore signalling for longer to the interior of the cell. This increases the sensitivity of cells to any hormones which might be present. The binding motif, of which this sequence is an example, is located at or around a ubiquitin and/or ubiquitin/proteosome complex binding site. The inhibitor of the method is either derived from, competes with, or binds to this binding motif. The inhibitor may be used to treat muscle wasting, associated with disorders such as renal tubular defects, uraemia, diabetes, Cushing's syndrome, cachexias, eating disorders, AIDS, after

26 39 70.9 321 2 AAW20847 H. pylori  
27 37 67.3 14 2 AAR40027 Chelator  
28 37 67.3 103 3 AAG43966 Zea mays  
29 37 67.3 103 3 AAG40846 Zea mays  
30 37 67.3 133 3 AAG43965 Zea mays  
31 37 67.3 650 3 AAG52494 Arabidops  
32 37 67.3 662 3 AAG52493 Arabidops  
33 37 67.3 675 3 AAG52492 Arabidops  
34 37 67.3 1298 2 AAR85937 Protein t  
35 37 67.3 1298 2 AAR90528 FLT4 rece  
36 37 67.3 1298 3 AAY90365 Human Flt  
37 37 67.3 1298 3 AAY70746 Human tyr  
38 37 67.3 1298 3 AAB30542 Amino aci  
39 37 67.3 1298 4 AAY97785 Mouse Flt  
40 37 67.3 1298 4 AAY97575 Human Flt  
41 37 67.3 1298 5 AEG32043 Human Flt  
42 37 67.3 1298 6 ABU07853 Human vas  
43 37 67.3 1298 6 ABU04292 Human exp  
44 37 67.3 1298 6 ABU04307 Human exp  
45 37 67.3 1298 6 ABU04298 Human exp

CC stress and during neuromuscular disease

XX Sequence 12 AA;

SQ Query Match 100.0%; Score 55; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10

DB 2 DSWVEFIELD 11

RESULT 2

AAAY32792

ID AAY32792 standard; peptide; 130 AA.

XX AC

XX AC AAY32792;

XX DT 09-NOV-1999 (first entry)

XX DE Growth hormone receptor polypeptide.

XX KW Signal transduction; proteolytic cleavage; growth hormone receptor;  
 KW proteosome binding site; muscle wasting; renal tubular defect; uraemia;  
 KW diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin;  
 KW growth hormone deficiency.

XX OS Mammalia.

XX PN EP943624-A1.

XX PD 22-SEP-1999.

XX PF 12-MAR-1998; 98EP-00200799.

XX PR 12-MAR-1998; 98EP-00200799.

XX PA (UYUT-) RIJKSUNIV UTRECHT.

XX DR WPI; 1999-510568/43.

XX PT Controlling the availability and/or signal transduction capability of a

XX PS cell surface receptor, useful for treating growth hormone deficiencies.

XX SQ Disclosure; Page 5; 36pp; English.

CC This sequence is a growth hormone receptor polypeptide. Polypeptides for

CC the upregulation of the growth hormone receptor are derived from this

CC sequence e.g. AAY32793. Variants (AAY32794-Y32823) of the derived

CC sequence are examples of polypeptide sequences found at or near the

CC ubiquitin/proteosome binding site located on the intracellular part of a

CC cell surface receptor. These sequences are used in a method for

CC controlling the availability and signal transduction capability of a cell

CC surface receptor by administering an inhibitor that is capable of

CC inhibiting proteolytic cleavage of the receptor. Inhibition of this

CC proteolytic cleavage results in the receptors being present on the

CC surface for longer and therefore signalling for longer to the interior of

CC the cell. This increases the sensitivity of cells to any hormones which

CC might be present. The inhibitor is either derived from, competes with or

CC binds to a polypeptide sequence of which sequences AAY32794-Y32823 are

CC examples. The inhibitor may be used to treat muscle wasting, associated

CC with disorders such as renal tubular defects, uraemia, diabetes,

CC Cushing's syndrome, cachexias, eating disorders, AIDS, after stress and

CC during neuromuscular disease

XX SQ Sequence 130 AA;

Query Match 100.0%; Score 55; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10

DB 53 DSWVEFIELD 62

RESULT 3

AAAP92108

ID AAP92108 standard; protein; 637 AA.

XX AC

XX AC AAP92108;

XX DT 14-FEB-1990 (first entry)

XX DE Human growth hormone receptor.

XX KW Growth hormone receptor.

XX OS Homo sapiens.

XX PN US4857637-A.

XX PD 15-AUG-1989.

XX PF 12-JUN-1987; 87US-00061942.

XX PR 22-MAY-1985; 85US-00737302.

XX PR 07-MAY-1986; 86US-00861236.

XX PA (GETH ) GENENTECH INC.

XX PI Hammonds RG, Leung DW, Martin DW, Spencer SA, Wood WI;

XX DR WPI; 1989-300419/41.

XX DR N-PSDB; AAN91325.

XX PT Modulating growth hormone receptor activity - by immunising animal

XX PT against growth hormone receptor extracellular domain deriv. to raise

XX PS antiserum.

XX PS Disclosure; Fig 2a-c; 18pp; English.

XX CC An animal can be immunised against its growth hormone receptor by

XX CC vaccinating against a growth hormone receptor extracellular domain deriv.

XX CC predetermined to raise polyclonal antisera which affect the receptor as a

XX CC growth hormone agonist. This method enables continuous growth of target

XX CC tissues without frequent hormone admin

XX SQ Sequence 637 AA;

Query Match 100.0%; Score 55; DB 1; Length 637;

Best Local Similarity 100.0%; Pred. No. 0.71;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10

DB 340 DSWVEFIELD 349

RESULT 4

AAAP81326

ID AAP81326 standard; protein; 638 AA.

XX AC

XX AC AAP81326;

XX DT 23-OCT-1990 (first entry)

XX DE Human growth hormone receptor.

XX KW Growth hormone receptor; gigantism; acromegaly.

XX OS Homo sapiens.

XX FH Key

FT Peptide

Location/Qualifiers

1. .18





Qy 1 DSWVEFIELD 10  
 |||||  
 Db 340 DSWVEFIELD 349

RESULT 7  
 AAW33394  
 ID AAW33394 standard; protein; 638 AA.

XX AC AAW33394;  
 XX XX 25-MAR-2003 (revised)  
 DT 11-MAY-1998 (first entry)  
 XX XX Human growth hormone receptor.

XX XX Growth hormone receptor; growth hormone binding protein; somatotropin;  
 KW human; gigantism; acromegaly; therapy.  
 XX OS Homo sapiens.

XX Key Location/Qualifiers  
 FT Peptide 1..18  
 FT /label= Sig\_peptide  
 FT Domain 247..269  
 FT /note= "transmembrane domain"  
 FT Misc-difference 375  
 FT /note= "translated codon is Ser in clone ghr.210 and  
 FT ghr.110, Ile in ghr.501"

XX US5688763-A.  
 XX 18-NOV-1997.

XX 25-MAY-1994; 94US-00248832.  
 XX 12-JUN-1987; 87US-00062542.  
 PR 28-JUN-1991; 91US-00723358.  
 PR 08-JAN-1993; 93US-00002489.

XX (LEUN/) LEUNG D W.  
 PA (HAMM/) HAMMONDS R G.  
 PA (WOOD/) WOOD W I.  
 PA (COLO/) COLOSI P C.  
 PA (SPEN/) SPENCER S A.

XX Colosi PC, Spencer SA, Leung DW, Hammonds RG, Wood WI;  
 WPI; 1998-008010/01.  
 DR N-PSDB; AAT94063.

XX Human and rabbit growth hormone receptor protein - useful to treat  
 PT disorders associated with overexpression, e.g. gigantism and acromegaly.  
 XX Claim 2; Fig 8a; 60pp; English.

XX This protein sequence comprises human growth hormone receptor. The amino  
 CC acid sequence was deduced from cDNA clones (see AAT94063) obtained from a  
 CC human liver cDNA library, and shows 84% identity to the rabbit growth  
 CC hormone receptor (see AAW33395). Human growth hormone receptor, its  
 CC derivatives in which the cytoplasmic or transmembrane domains are  
 CC deleted, and growth hormone binding proteins comprising amino acids 190-  
 CC 246 or 1-324 of the mature protein, can be used to treat disorders  
 CC associated with growth hormone over-expression, e.g. gigantism and  
 CC acromegaly. The binding protein may also be used to increase the  
 CC stability and efficacy of growth hormone in vivo. (Updated on 25-MAR-2003  
 CC to correct PF field.)

XX Sequence 638 AA;

Query Match 100.0%; Score 55; DB 2; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 0.71;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10  
 |||||  
 Db 340 DSWVEFIELD 349

RESULT 8  
 AAW33395  
 ID AAW33395 standard; protein; 638 AA.

XX AC AAW33395;  
 XX XX 25-MAR-2003 (revised)  
 DT 11-MAY-1998 (first entry)  
 XX XX Rabbit growth hormone receptor.

XX XX Growth hormone receptor; growth hormone binding protein; somatotropin;  
 KW rabbit; gigantism; acromegaly; therapy.  
 XX OS Oryctolagus cuniculus.

XX Key Location/Qualifiers  
 FT Peptide 1..18  
 FT /label= Sig\_peptide  
 FT Misc-difference 49  
 FT /note= "translated codon is Ala in clone ghr.435, Thr in  
 FT ghr.440"  
 FT Domain 247..269  
 FT /note= "transmembrane domain"

XX US5688763-A.  
 XX 18-NOV-1997.

XX 25-MAY-1994; 94US-00248832.  
 XX 12-JUN-1987; 87US-00062542.  
 PR 28-JUN-1991; 91US-00723358.  
 PR 08-JAN-1993; 93US-00002489.

XX (LEUN/) LEUNG D W.  
 PA (HAMM/) HAMMONDS R G.  
 PA (WOOD/) WOOD W I.  
 PA (COLO/) COLOSI P C.  
 PA (SPEN/) SPENCER S A.

XX Colosi PC, Spencer SA, Leung DW, Hammonds RG, Wood WI;  
 WPI; 1998-008010/01.  
 DR N-PSDB; AAT94064.

XX Human and rabbit growth hormone receptor protein - useful to treat  
 PT disorders associated with overexpression, e.g. gigantism and acromegaly.  
 XX Claim 2; Fig 8b; 60pp; English.

XX This protein sequence comprises rabbit growth hormone receptor. The amino  
 CC acid sequence was deduced from cDNA clones (see AAT94064) obtained from a  
 CC rabbit liver cDNA library, and shows 84% identity to the human growth  
 CC hormone receptor (see AAW33394). Rabbit and human growth hormone  
 CC receptors, their derivatives in which the cytoplasmic or transmembrane  
 CC domains are deleted, and growth hormone binding proteins comprising amino  
 CC acids 190-246 or 1-324 of the mature proteins, can be used to treat  
 CC disorders associated with growth hormone over-expression, e.g. gigantism  
 CC and acromegaly. The binding protein may also be used to increase the  
 CC stability and efficacy of growth hormone in vivo. (Updated on 25-MAR-2003  
 CC to correct PF field.)

XX Sequence 638 AA;

Query Match 100.0%; Score 55; DB 2; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 0.71;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVERFIELD 10  
Best Local Similarity 100.0%; Score 55; DB 7; Length 638;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 340 DSWVERFIELD 349  
|||||

RESULT 9  
ADD45061  
ID ADD45061 standard; protein; 638 AA.  
XX AC ADD45061;  
XX  
XX 29-JAN-2004 (first entry)  
XX  
DE Rat Protein P16310, SEQ ID NO 10493.  
XX  
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
OS Rattus norvegicus.  
XX  
PN WO2003016475-A2.  
XX  
XX 27-FEB-2003.  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (PARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX WPI: 2003-268312/26.  
XX GENBANK; P16310.  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 638 AA;

Query Match 100.0%; Score 55; DB 7; Length 638;  
Best Local Similarity 100.0%; Pred. No. 0.71;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVERFIELD 10  
|||||

Db 341 DSWVERFIELD 350  
|||||

RESULT 10  
ADD45067  
ID ADD45067 standard; protein; 638 AA.  
XX AC ADD45067;  
XX  
XX 29-JAN-2004 (first entry)  
XX  
DE Human Protein P10912, SEQ ID NO 10499.  
XX  
XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016475-A2.  
XX  
XX 27-FEB-2003.  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
XX  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (PARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX WPI: 2003-268312/26.  
XX GENBANK; P10912.  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification).

CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 638 AA;

Query Match 100.0%; Score 55; DB 7; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 0.71; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0;

Qy 1 DSWVEFIELD 10  
 |||||  
 Db 340 DSWVEFIELD 349

RESULT 11

ADD45063  
 ID ADD45063 standard; protein; 638 AA.

XX AC ADD45063;

XX DT 29-JAN-2004 (first entry)

XX DE Human Protein P10912, SEQ ID NO 10495.

XX KW Human; pain; neuronal tissue; gene therapy;

XX KW spinal segmental nerve injury; chronic constriction injury; CCI;

XX KW spared nerve injury; SNI; Chung.

XX OS Homo sapiens.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO ) GEN HOSPITAL CORP.

XX PA (FARB ) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX DR GENBANK; P10912.

XX PT New composition comprising two or more isolated polypeptides, useful for  
 XX preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC Claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 638 AA;

Query Match 100.0%; Score 55; DB 7; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 0.71;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10  
 |||||  
 Db 340 DSWVEFIELD 349

RESULT 12

ADD45065  
 ID ADD45065 standard; protein; 638 AA.

XX AC ADD45065;

XX DT 29-JAN-2004 (first entry)

XX DE Rat Protein P16310, SEQ ID NO 10497.

XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS Rattus norvegicus.

XX PN WO2003016475-A2.

XX PD 27-FEB-2003.

XX PF 14-AUG-2002; 2002WO-US025765.

XX PR 14-AUG-2001; 2001US-0312147P.

XX PR 01-NOV-2001; 2001US-0346382P.

XX PR 26-NOV-2001; 2001US-0333347P.

XX PA (GEHO ) GEN HOSPITAL CORP.

XX PA (FARB ) BAYER AG.

XX PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX DR GENBANK; P16310.

XX PT New composition comprising two or more isolated polypeptides, useful for  
 XX preparing a medicament for treating pain in an animal.

XX PS Claim 1; Page; 1017pp; English.

XX CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC Claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a

method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 638 AA;

Query Match 100.0%; Score 55; DB 7; Length 638;  
Best Local Similarity 100.0%; Pred. No. 0.71;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10  
Db 341 DSWVEFIELD 350  
|||||

RESULT 13

AB811437  
ID ABB11437 standard; peptide; 648 AA.

XX AC ABB11437;

XX 11-JAN-2002 (first entry)

DE Human growth hormone receptor homologue, SEQ ID NO:1807.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor;  
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;  
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
KW chronic inflammatory condition; proliferative retinopathy;  
KW atherosclerosis; coronary heart disease; arterial ischaemia;  
KW bone disorder; osteoporosis; vascular growth disorder;  
KW tissue regeneration; wound healing; infection; immune disorder;  
KW cell culture; drug screening; gene therapy; antiinflammatory;  
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
KW cytotatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;  
KW antifungal; vulnery; antiulcer.

XX Homo sapiens.

XX WC200157188-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US03800.

XX 03-FEB-2000; 2000US-00496914.

XX 27-APR-2000; 2000US-00560875.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-457740/49.

XX N-PSDB; ABA08681.

XX Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer.

XX Claim 20; Page 189-190; 1963pp; English.

CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
CC invention also relates to vectors and recombinant host cells comprising a  
CC nucleotide of the invention, methods of producing the novel polypeptides,  
CC antibodies against the polypeptides, methods of detecting the nucleotides,  
CC or polypeptides in a sample, and methods of identifying compounds which  
CC bind to polypeptides of the invention. Although novel, many of the  
CC polypeptides of the invention have homology to known proteins, thereby  
CC giving an insight into their probable biological activities, and hence  
CC potential therapeutic applications. The polypeptides of the invention may  
CC have various activities, including cytokine, cell proliferation or cell  
CC differentiation activities; stem cell growth factor activity;  
CC haematopoiesis regulatory activity; tissue growth activity;  
CC immunomodulatory activity; activin- or inhibin-related activities;  
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
CC thrombolytic activities; receptor or ligand activities; or may be  
CC involved in oncogenesis, cancer cell proliferation or metastasis.  
CC Depending on their biological activities, polypeptides and nucleotides of  
CC the invention are useful for preventing, treating or ameliorating medical  
CC conditions, e.g., by protein or gene therapy. Such conditions include  
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
CC vascular growth. Polypeptides involved with tissue regeneration and  
CC repair (or nucleic acids encoding them) may be used to promote wound  
CC healing (e.g., of burns, incisions and ulcers), while those with  
CC immunomodulatory activities may be used in the treatment of viral,  
CC bacterial and fungal infections in addition to immune disorders.  
CC Polypeptides with growth factor activity may be used in cell cultures to  
CC promote cell growth. For example, such polypeptides may be used to  
CC manipulate stem cells in culture to give rise to neuroepithelial cells  
CC that can be used to augment or replace cells damaged by illness,  
CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
CC may also be used in the diagnosis of the above conditions, and in drug  
CC screening techniques. The present sequence represents a novel human  
CC polypeptide of the invention

XX Sequence 648 AA;

Query Match 100.0%; Score 55; DB 4; Length 648;  
Best Local Similarity 100.0%; Pred. No. 0.72;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10  
Db 350 DSWVEFIELD 359  
|||||

RESULT 14

AAR06473  
ID AAR06473 standard; protein; 638 AA.

XX AC AAR06473;

XX 27-AUG-2003 (revised)

DT 04-JAN-1991 (first entry)

XX Serum somatotropin receptor protein from clone pRAT7-12.

DE Somatotropin receptor; SR; somatotropin binding protein; SBP; pRAT7-12;  
KW pRAT1-6.

XX Rattus rattus.

XX Key Location/Qualifiers

FT Peptide 1..17 /label= signal\_sequence

FT Region 262..638 /label= divergence

FT /note= "non-homology region with SBP/pRAT1-6"

FT Domain 264..289

FT /label= transmembrane\_domain

XX EP383205-A.  
 XX 22-AUG-1990.  
 PD 09-FEB-1990; 90EP-00102552.  
 XX 17-FEB-1989; 89US-00310725.  
 XX (AMCY ) AMERICAN CYANAMID CO.  
 XX Logan JS, Baumbach WR;  
 XX WPI; 1990-255493/34.  
 XX N-PSDB; AAQ05691.  
 XX Somatotropin binding protein and gene - used to regulate and/or modify  
 PT activity of somatotropin in humans and animals.  
 XX Disclosure; Fig 6; 43pp; English.  
 XX Homology comparison between this putative rat somatotropin receptor and  
 CC the published sequence indicates 70% identity. See also AAQ05689-91,  
 CC AAQ06124 and AAQ05700. (Updated on 27-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 638 AA;  
 Query Match 92.7%; Score 51; DB 2; Length 638;  
 Best Local Similarity 90.0%; Pred. No. 3.3;  
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSWVEFIELD 10  
 Db 341 ESWVEFIELD 350  
 RESULT 15  
 AAAY32793  
 ID AAAY32793 standard; peptide; 12 AA.  
 XX  
 AC AAAY32793;  
 XX  
 DT 09-NOV-1999 (first entry)  
 XX  
 DE Growth hormone receptor derived polypeptide.  
 XX  
 KW Signal transduction; proteolytic cleavage; growth hormone receptor;  
 KW proteosome binding site; muscle wasting; renal tubular defect; uraemia;  
 KW diabetes; Cushing's disease; eating disorder; AIDS; ubiquitin;  
 KW growth hormone deficiency.  
 XX  
 OS Mammalia.  
 XX  
 PN EP943624-A1.  
 XX  
 PD 22-SEP-1999.  
 XX  
 PF 12-MAR-1998; 98EP-00200799.  
 XX  
 PR 12-MAR-1998; 98EP-00200799.  
 XX  
 PA (UYUT-) RIJKSUNIV UTRECHT.  
 XX  
 DR WPI; 1999-510568/43.  
 XX  
 PT Controlling the availability and/or signal transduction capability of a  
 PT cell surface receptor, useful for treating growth hormone deficiencies.  
 XX  
 PS Disclosure; Page 5; 36pp; English.  
 XX  
 CC This sequence is derived from the growth hormone receptor polypeptide  
 CC AAAY32792. This sequence and variants (AAAY32794-Y32823) of it are examples  
 CC of polypeptide sequences found at or near the ubiquitin/proteosome

CC binding site located on the intracellular part of a cell surface  
 CC receptor. These sequences are used in a method for controlling the  
 CC availability and signal transduction capability of a cell surface  
 CC receptor by administering an inhibitor that is capable of inhibiting  
 CC proteolytic cleavage of the receptor. Inhibition of this proteolytic  
 CC cleavage results in the receptors being present on the surface for longer  
 CC and therefore signalling for longer to the interior of the cell. This  
 CC increases the sensitivity of cells to any hormones which might be  
 CC present. The inhibitor is either derived from, competes with or binds to  
 CC a polypeptide sequence of which sequences AAAY32794-Y32823 are examples.  
 CC The inhibitor may be used to treat muscle wasting, associated with  
 CC disorders such as renal tubular defects, uraemia, diabetes, Cushing's  
 CC syndrome, cachexias, eating disorders, AIDS, after stress and during  
 CC neuromuscular disease  
 XX  
 SQ Sequence 12 AA;  
 Query Match 89.1%; Score 49; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.11;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SWVEFIELD 10  
 Db 1 SWVEFIELD 9  
 Search completed: June 9, 2004, 15:48:27  
 Job time : 51 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2004, 15:43:40 ; Search time 11.0811 Seconds  
(without alignments)  
86.807 Million cell updates/sec

Title: US-09-660-302D-3

Perfect score: 55

Sequence: 1 DSWVEFIELD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR.78.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	634	2 S33339	somatotropin recep
2	55	100.0	638	2 A33505	somatotropin recep
3	55	100.0	638	2 A33991	somatotropin recep
4	55	100.0	638	2 B28176	somatotropin recep
5	55	100.0	638	2 S12136	somatotropin recep
6	55	100.0	677	2 S33608	somatotropin-bind
7	49	89.1	608	2 S32823	somatotropin recep
8	46	83.6	702	2 A61619	arylphorin precurs
9	41	74.5	704	2 A34287	storage protein 2
10	41	74.5	1379	2 JC4954	vascular endotheli
11	40	72.7	1363	2 I58375	protein-tyrosine k
12	39	70.9	217	2 AG2426	hypothetical prote
13	39	70.9	321	2 H71924	hypothetical prote
14	39	70.9	321	2 B64589	hypothetical prote
15	39	70.9	411	2 B66916	hypothetical prote
16	38	69.1	103	2 T03951	signal recognition
17	37	67.3	363	2 S75238	hypothetical prote
18	37	67.3	840	2 T36175	probable large ATP
19	37	67.3	1298	2 A48999	protein-tyrosine k
20	36	65.5	208	2 B87468	conserved hypothet
21	36	65.5	243	2 B69951	hypothetical prote
22	36	65.5	268	2 T50354	5-amino-6-(5-phosp
23	36	65.5	316	2 C88448	protein C45G9.5 [i
24	36	65.5	399	2 A97993	nikkomycin biosynt
25	36	65.5	694	2 S67396	probable membrane
26	36	65.5	718	2 T05850	homeobox protein A
27	35	63.6	155	2 S70046	hypothetical prote
28	35	63.6	210	2 S74784	hypothetical prote
29	35	63.6	259	2 A59095	hypothetical prote

30	35	63.6	297	2 G84731	hypothetical prote
31	35	63.6	387	2 T29966	hypothetical prote
32	35	63.6	456	2 T48291	hypothetical prote
33	35	63.6	525	2 S35614	site-specific DNA-
34	35	63.6	537	2 T21823	hypothetical prote
35	35	63.6	544	2 F82557	hypothetical prote
36	35	63.6	555	2 T00778	probable tRNA aden
37	35	63.6	572	2 D95174	phosphoglucomutase
38	35	63.6	572	2 F98040	phosphomannomutase
39	35	63.6	599	2 T5742	crooked neck-like
40	35	63.6	621	2 A57591	Id-associated prot
41	35	63.6	721	2 C84732	probable homeodoma
42	35	63.6	749	2 G86186	hypothetical prote
43	35	63.6	800	2 S13032	3',5'-cyclic-GMP p
44	35	63.6	853	2 A36617	3',5'-cyclic-GMP p
45	35	63.6	854	2 A42828	3',5'-cyclic-GMP p

## ALIGNMENTS

### RESULT 1

S33339

somatotropin receptor - sheep

N;Alternate names: growth hormone receptor

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 08-Dec-1993 #sequence\_revision 01-Dec-1995 #text\_change 02-Aug-2002

C;Accession: S33339

R;Adams, T.E.; Baker, L.; Fiddes, R.J.; Brandon, M.R.

Mol. Cell. Endocrinol. 73, 135-145, 1990

A;Title: The sheep growth hormone receptor: molecular cloning and ontogeny of mRNA expr

A;Reference number: S33339; MUID:91099608; PMID:1980117

A;Accession: S33339

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-634 <ADA>

A;Cross-references: EMBL:M02912; NID:g165888; PIDN:AAA73171.1; PID:g165889

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

Query Match 100.0%; Score 55; DB 2; Length 634;

Best Local Similarity 100.0%; Pred. NO. 0.05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10

Db 336 DSWVEFIELD 345

### RESULT 2

A33505

somatotropin receptor precursor - rat

N;Alternate names: growth hormone receptor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Nov-1989 #sequence\_revision 22-Nov-1989 #text\_change 02-Aug-2002

C;Accession: A32985; A33505

R;Baumbach, W.R.; Horner, D.L.; Logan, J.S.

Genes Dev. 3, 1199-1205, 1989

A;Title: The growth hormone-binding protein in rat serum is an alternatively spliced fo

A;Reference number: A32985; MUID:90006741; PMID:2792761

A;Accession: A32985

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-638 <BAU>

A;Cross-references: GB:X16726

R;Mathews, L.S.; Enberg, B.; Norstedt, G.

J. Biol. Chem. 264, 9905-9910, 1989

A;Title: Regulation of rat growth hormone receptor gene expression.

A;Reference number: A33505; MUID:89255563; PMID:2722883

A;Accession: A33505

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-638 <MAT>

A;Cross-references: GB:J04811; NID:g204308; PIDN:AAA41219.1; PID:g204309

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology  
C;Keywords: transmembrane protein

Query Match 100.0%; Score 55; DB 2; Length 638;  
Best Local Similarity 100.0%; Pred. No. 0.051;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10  
|||||

Db 341 DSWVEFIELD 350

## RESULT 3

A33991  
somatotropin receptor precursor - human  
N;Alternate names: growth hormone receptor  
C;Species: Homo sapiens (man)  
C;Date: 23-Mar-1990 #sequence\_revision 23-Mar-1990 #text\_change 02-Aug-2002  
C;Accession: A33991; S04530

R;Godowski, P.J.; Leung, D.W.; Meacham, L.R.; Galgani, J.P.; Hellmiss, R.; Keret, R.; R  
Proc. Natl. Acad. Sci. U.S.A. 86, 8083-8087, 1989  
A;Title: Characterization of the human growth hormone receptor gene and demonstration of  
A;Reference number: A33991; MUID:90046742; PMID:2813379

A;Accession: A33991

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-638 <GOD>

A;Cross-references: GB:M28458; GB:M28459; GB:M28460; GB:M28461; GB:M28462; GB:M28463; GB  
R;Leung, D.W.; Spencer, S.A.; Cachianes, G.; Hammonds, R.G.; Collins, C.; Henzel, W.J.;  
Nature 330, 537-543, 1987

A;Title: Growth hormone receptor and serum binding protein: purification, cloning and ex  
A;Reference number: S04530; MUID:88065896; PMID:2825030

A;Accession: S04530

A;Molecule type: mRNA

A;Residues: 1-543; 'I', 545-638 <LEU>

A;Cross-references: EMBL:X06562; NID:G31737; PIDN:CAA29808.1; PID:G31738

C;Genetics:

A;Gene: GDB:GHR

A;Cross-references: GDB:119984; OMIM:600946

A;Map position: Spi3-Spi2

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology  
C;Keywords: liver; transmembrane protein

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-638/Product: somatotropin receptor #status predicted <MAT>

F;265-288/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 55; DB 2; Length 638;

Best Local Similarity 100.0%; Pred. No. 0.051;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10

|||||

Db 340 DSWVEFIELD 349

## RESULT 4

B28176  
somatotropin receptor precursor, hepatic - rabbit  
N;Alternate names: growth hormone receptor  
C;Species: somatotropin-binding protein, serum  
C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 28-Feb-1990 #sequence\_revision 10-Mar-1994 #text\_change 02-Aug-2002

C;Accession: S08544; B28176; A28176

R;Leung, D.W.; Spencer, S.A.; Cachianes, G.; Hammonds, R.G.; Collins, C.; Henzel, W.J.;

Nature 330, 537-543, 1987

A;Title: Growth hormone receptor and serum binding protein: purification, cloning and ex  
A;Reference number: S04530; MUID:88065896; PMID:2825030

A;Accession: S08544

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-638 <LEU>

A;Cross-references: GB:AF015252; NID:G2342651; PIDN:AAB67613.1; PID:G2342652

A;Note: part of this sequence, including the amino end of the mature protein, was confi  
R;Spencer, S.A.; Hammonds, R.G.; Henzel, W.J.; Rodriguez, H.; Waters, M.J.; Wood, W.I.  
J. Biol. Chem. 263, 7862-7867, 1988

A;Title: Rabbit liver growth hormone receptor and serum binding protein. Purification,  
A;Reference number: A92721; MUID:88227992; PMID:3372509

A;Accession: B28176

A;Molecule type: protein

A;Residues: 19-34; 'SPG', 81-88; 'X', 99, 'XX', 102-105, 'X', 107-110, 'XX', 113-114, 'X', 141, 'X',  
-574, 'X', 576-577; 579-595 <SPE>

A;Note: sequence is derived from intact receptor

A;Accession: A28176

A;Molecule type: protein

A;Residues: 'XXX', 22-45, 'X', 47-55 <SP2>

A;Note: sequence is derived from a soluble form of the receptor isolated from serum  
C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

C;Keywords: glycoprotein; liver; transmembrane protein

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-638/Product: somatotropin receptor #status experimental <MAT>

F;265-288/Domain: transmembrane #status predicted <TMM>

F;46,200/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 55; DB 2; Length 638;

Best Local Similarity 100.0%; Pred. No. 0.051;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10

|||||

Db 340 DSWVEFIELD 349

## RESULT 5

S12136  
somatotropin receptor precursor - pig  
N;Alternate names: growth hormone receptor  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 02-Aug-2002  
C;Accession: S12136

R;Cioffi, J.A.; Wang, X.; Kopchick, J.J.

Nucleic Acids Res. 18, 6451, 1990

A;Title: Porcine growth hormone receptor cDNA sequence.

A;Reference number: S12136; MUID:91057155; PMID:2243805

A;Accession: S12136

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-638 <C10>

A;Cross-references: EMBL:X54429; NID:G2037; PIDN:CAA38301.1; PID:G2038

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology  
C;Keywords: transmembrane protein

Query Match 100.0%; Score 55; DB 2; Length 638;

Best Local Similarity 100.0%; Pred. No. 0.051;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10

|||||

Db 340 DSWVEFIELD 349

## RESULT 6

S33608  
somatotropin-binding protein, high molecular weight, precursor - mouse  
N;Alternate names: growth hormone-binding protein, high molecular weight  
C;Species: Mus musculus (house mouse)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 02-Aug-2002

C;Accession: S33608; S33607

R;Smith, W.C.; Kuniyoshi, J.; Talamantes, F.

Mol. Endocrinol. 3, 984-990, 1989

A;Title: Mouse serum growth hormone (GH) binding protein has GH receptor extracellular  
A;Reference number: S33607; MUID:89295449; PMID:2739661

A;Accession: S33608

A;Molecule type: mRNA

A;Residues: 1-677 <SM1>

A;Cross-references: EMBL:M33324; NID:g193508; PIDN:AAA37690.1; PID:G309253



A;Experimental source: liver

A;Accession: S33607

A;Molecule type: mRNA

A;Residues: 1-324 <SM2>

A;Cross-references: EMBL:M31680; NID:g133506; PIDN:AAA37689.1; PID:g309252

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

C;Keywords: glycoprotein; receptor; transmembrane protein

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-677/Product: somatotropin-binding protein, high molecular weight #status predicted

F;274-297/Domain: transmembrane #status predicted <TM>

F;40,164,169/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;164,169/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 55; DB 2; Length 677;

Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10

|||||

Db 376 DSWVEFIELD 385

RESULT 7

S32823

somatotropin receptor precursor, major splice form - chicken

N;Alternate names: growth hormone receptor

N;Contains: somatotropin receptor, short form

C;Species: Gallus gallus (chicken)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 02-Aug-2002

C;Accession: S32823; A49812

R;Burnside, J.; Liou, S.S.; Cogburn, L.A.

Endocrinology 128, 3183-3192, 1991

A;Title: Molecular cloning of the chicken growth hormone receptor complementary deoxyribonucleic acid

A;Reference number: S32823; MUID:91243665; PMID:2036984

A;Accession: S32823

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-608 <BUR>

A;Cross-references: EMBL:M74057; NID:g211810; PIDN:AAA48781.1; PID:g211811

R;Huang, N.; Cogburn, L.A.; Agarwal, S.K.; Marks, H.L.; Burnside, J.

Mol. Endocrinol. 7, 1391-1398, 1993

A;Title: Overexpression of a truncated growth hormone receptor in the sex-linked dwarf d

A;Reference number: A49812; MUID:94158898; PMID:8114754

A;Accession: A49812

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-109 <HUA>

A;Cross-references: GB:S68576; NID:g499137; PIDN:AAB29983.1; PID:g499138

A;Experimental source: liver, normal chicken

A;Note: this truncated form is a minor splice form in normal chickens and the major form

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

C;Keywords: alternative splicing; receptor; sex-linked inheritance; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-109/Product: somatotropin receptor, short form #status predicted <SHO>

Query Match 89.1%; Score 49; DB 2; Length 608;

Best Local Similarity 90.0%; Pred. No. 0.58;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10

|||||

Db 313 DLWVEFIELD 322

RESULT 8

A61619

arylphorin precursor - greater wax moth

N;Alternate names: phenylalanine-rich protein Lhp76

C;Species: Galleria mellonella (greater wax moth)

C;Date: 21-Jul-1995 #sequence\_revision 11-Aug-1995 #text\_change 24-Sep-1999

C;Accession: A61619

R;Mummel, N.A.; Trewitt, P.M.; Silhacek, D.L.; Kumaran, A.K.

Insect Biochem. Mol. Biol. 22, 333-342, 1992

A;Title: Nucleotide sequence and structure of the arylphorin gene from Galleria mellone

A;Reference number: A61619

A;Accession: A61619

A;Molecule type: DNA

A;Residues: 1-702 <MEM>

A;Cross-references: GB:M73793; NID:g159077; PIDN:AAA74229.1; PID:g159078

A;Note: in the authors' translation, residue 306-Leu is omitted, residue 317-Asn is dup

C;Genetics:

A;Introns: 30/1; 74/3; 352/3; 410/2

A;Note: single copy gene

C;Superfamily: arylphorin

C;Keywords: glycoprotein; hemolymph; storage protein

F;1-16/Domain: signal sequence #status predicted <SIG>

F;211,481/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 83.6%; Score 46; DB 2; Length 702;

Best Local Similarity 70.0%; Pred. No. 2.3;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10

|||||

Db 547 DWINFIELD 556

RESULT 9

A34287

storage protein 2 - silkworm

C;Species: Bombyx mori (silkworm)

C;Date: 08-Jun-1990 #sequence\_revision 08-Jun-1990 #text\_change 04-Sep-1998

C;Accession: A34287

R;Fujii, T.; Sakurai, H.; Izumi, S.; Tomino, S.

J. Biol. Chem. 264, 11020-11025, 1989

A;Title: Structure of the gene for the arylphorin-type storage protein SP 2 of Bombyx mori

A;Reference number: A34287; MUID:89291839; PMID:2544581

A;Accession: A34287

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-704 <FUJ>

C;Superfamily: arylphorin

Query Match 74.5%; Score 41; DB 2; Length 704;

Best Local Similarity 60.0%; Pred. No. 19;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10

|||||

Db 544 DNMKFFELD 553

RESULT 10

JC4954

vascular endothelial growth factor receptor 2 precursor - Japanese quail

N;Alternate names: Quail endothelial kinase 2; Quek 2

C;Species: Coturnix coturnix japonica (Japanese quail)

C;Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 24-Sep-1999

C;Accession: JC4954

R;Eichmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.

Gene 174, 3-8, 1996

A;Title: Molecular cloning of Quek 1 and 2, two quail vascular endothelial growth factor

A;Reference number: JC4953; MUID:97017121; PMID:8863722

A;Accession: JC4954

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1379 <EIC>

A;Cross-references: EMBL:X83287; NID:g619865; PIDN:CAA58267.1; PID:e283815; PID:g1707419

C;Comment: This protein is an endothelial-specific receptor and binds vascular endothelial

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

C;Keywords: ATP; embryo; growth factor receptor; transmembrane protein

F;1-20/Domain: signal sequence #status predicted <SIG>

F;789-810/Domain: transmembrane #status predicted <TM>

F;856-1188/Domain: protein kinase homology <KIN>

F;864-872/Region: protein kinase ATP-binding motif

Query Match 74.5%; Score 41; DB 2; Length 1379;  
 Best Local Similarity 75.0%; Pred. No. 38;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIE 8  
 |||||  
 Db 519 DTWVEFVE 526

## RESULT 11

I58375  
 C:Species: protein-tyrosine kinase (EC 2.7.1.112) flt4 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 04-Feb-2000  
 C:Accession: I58375; B42010  
 R:Finerty, H.; Kelleher, K.; Morris, G.E.; Bean, K.; Merberg, D.M.; Kriz, R.; Morris, J.  
 Oncogene 8, 2293-2298, 1993  
 A:Title: Molecular cloning of murine FLT and FLT4.  
 A:Reference number: I58375; MUID:93330572; PMID:8393164  
 A:Accession: I58375  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1363 <RES>  
 A:Cross-references: GB:I07296; NID:G293780; PIDN:AAA40077.1; PID:G293781  
 R:Galland, F.; Karamysheva, A.; Mattei, M.G.; Rosnet, O.; Marchetto, S.; Birnbaum, D.  
 Genomics 13, 475-478, 1992  
 A:Title: Chromosomal localization of FLT4, a novel receptor-type tyrosine kinase gene.  
 A:Reference number: A42010; MUID:92307693; PMID:11319394  
 A:Accession: B42010  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: DNA  
 A:Residues: 1033-1072 <GAL>  
 C:Genetics:  
 A:Gene: FLT4  
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo  
 C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase  
 F:843-1176/Domain: protein kinase homology <KIN>  
 F:851-859/Region: protein kinase ATP-binding motif

Query Match 72.7%; Score 40; DB 2; Length 1363;  
 Best Local Similarity 75.0%; Pred. No. 57;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DSWVEFIE 8  
 |||||  
 Db 505 DSWTEFVE 512

## RESULT 12

AG2426  
 C:Species: Nostoc sp. PCC 7120  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
 R:Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuguchi  
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AG2426  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-217 <KUR>  
 A:Cross-references: GB:BA000019; PIDN:BA876666.1; PID:gl71341105; GSPDB:GN00179  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: all4967

Query Match 70.9%; Score 39; DB 2; Length 217;  
 Best Local Similarity 87.5%; Pred. No. 12;  
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WVEFIELD 10  
 |||||  
 Db 182 WVEFIELD 189

## RESULT 13

H71924  
 C:Species: Helicobacter pylori (strain J99)  
 A:Variety: strain J99  
 C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 28-Jul-2000  
 C:Accession: H71924  
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
 Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
 Nature 397, 176-180, 1999  
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pat  
 A:Reference number: A71800; MUID:99120557; PMID:9923682  
 A:Accession: H71924  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-321 <ARN>  
 A:Cross-references: GB:AE001483; GB:AE001439; NID:94155034; PIDN:AAD06079.1; PID:941550  
 A:Experimental source: strain J99  
 C:Genetics:  
 A:Gene: jhp0501  
 C:Superfamily: Helicobacter pylori hypothetical protein jhp0501

Query Match 70.9%; Score 39; DB 2; Length 321;  
 Best Local Similarity 70.0%; Pred. No. 18;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10  
 |||||  
 Db 240 DIWVEVIDLD 249

## RESULT 14

B64589  
 C:Species: Helicobacter pylori  
 C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 28-Jul-2000  
 C:Accession: B64589  
 R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.  
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn  
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L  
 Nature 388, 539-547, 1997  
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
 A:Reference number: A64520; MUID:97394467; PMID:9252185  
 A:Accession: B64589  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-321 <TOM>  
 A:Cross-references: GB:AE000569; GB:AE000511; NID:92313663; PIDN:AAD07620.1; PID:923136  
 C:Superfamily: Helicobacter pylori hypothetical protein jhp0501

Query Match 70.9%; Score 39; DB 2; Length 321;  
 Best Local Similarity 70.0%; Pred. No. 18;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10  
 |||||  
 Db 240 DIWVEVIDLD 249

## RESULT 15

S66916  
 C:Species: Saccharomyces cerevisiae  
 A:Alternate names: hypothetical protein O2762  
 C:Species: Saccharomyces cerevisiae  
 C:Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 19-Apr-2002  
 C:Accession: S66916  
 R:Landt, O.; Hiesel, R.; Unseld, M.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S66907  
 A;Accession: S66916  
 A;Molecule type: DNA  
 A;Residues: 1-411 <LAN>  
 A;Cross-references: EMBL:Z74949; NID:gl420165; PID:e251966; PID:gl420167; GSPDB:GN000015;  
 A;Experimental source: strain S288C  
 C;Genetics:  
 A;Gene: MIPS:YOR042w  
 A;Cross-references: SGD:S0005568  
 A;Map position: 15R

Query Match 70.9%; Score 39; DB 2; Length 411;  
 Best Local Similarity 60.0%; Pred. No. 24;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10  
 ||| :|||  
 Db 224 DSWSQFVEKD 233

Search completed: June 9, 2004, 15:52:17  
 Job time : 12.0811 secs

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: June 9, 2004, 15:36:55 ; Search time 7.2973 Seconds  
(without alignments)  
71.355 Million cell updates/sec

Title: US-09-660-302D-3  
Perfect score: 55  
Sequence: 1 DSWVEFIELD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	55	100.0	634	1	GHR_BOVIN
2	55	100.0	634	1	GHR_SHEEP
3	55	100.0	638	1	GHR_HUMAN
4	55	100.0	638	1	GHR_MACMU
5	55	100.0	638	1	GHR_PIG
6	55	100.0	638	1	GHR_RABIT
7	55	100.0	638	1	GHR_RAT
8	55	100.0	650	1	GHR_MOUSE
9	49	89.1	608	1	GHR_CHICK
10	49	89.1	611	1	GHR_COLLI
11	42	76.4	1409	1	RPOC_PSEPU
12	41	74.5	704	1	SSP2_BOMMO
13	40	72.7	1363	1	VGR3_MOUSE
14	38	69.1	103	1	SR09_MAIZE
15	37	67.3	341	1	MURB_SHEON
16	37	67.3	1298	1	VGR3_HUMAN
17	36	65.5	243	1	YQEF_BACSV
18	36	65.5	316	1	VQ15_CAEEL
19	36	65.5	358	1	V4FP_RHISN
20	36	65.5	358	1	FRES_YEAST
21	35	63.6	514	1	ZRF1_MOUSE
22	35	63.6	521	1	MTAL_ARTLU
23	35	63.6	533	1	UGT5_CAEEL
24	35	63.6	568	1	ZRF1_HUMAN
25	35	63.6	690	1	CRN1_MOUSE
26	35	63.6	848	1	CRN1_HUMAN
27	35	63.6	853	1	CNRB_BOVIN
28	35	63.6	854	1	CNRB_HUMAN
29	35	63.6	856	1	CNRB_CANFA
30	35	63.6	856	1	CNRB_MOUSE
31	34.5	62.7	3707	1	PGBM_MOUSE
32	34.5	62.7	4391	1	PGBM_HUMAN
33	34	61.8	80	1	RUB1_METJA

34	34	61.8	122	1	RFA3_YEAST	P26755	saccharomyc
35	34	61.8	447	1	HST3_YEAST	P53687	saccharomyc
36	34	61.8	476	1	UGDH_DROME	O02373	drosophila
37	34	61.8	498	1	GTA_NPVOP	O10302	orgyia pseu
38	34	61.8	983	1	ESYN_GIBPU	Q00868	gibberella
39	34	61.8	1094	1	YB00_YEAST	P38114	saccharomyc
40	34	61.8	1163	1	ITAL_MOUSE	P24063	mus musculus
41	33.5	60.9	788	1	SYFB_THEMEA	Q9WZS9	thermotoga
42	33	60.0	75	1	S100_LEPPA	P82978	lepidosiren
43	33	60.0	123	1	DESR_DESYM	P48345	desulfovibr
44	33	60.0	125	1	DESR_DESDE	P22076	desulfovibr
45	33	60.0	125	1	DESR_DESVH	P20418	desulfovibr

## ALIGNMENTS

### RESULT 1

ID	GHR_BOVIN	STANDARD	PRT	634 AA.
AC	P79108;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Growth hormone receptor precursor (GH receptor) (Serum binding protein).			
DE	GHR.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.			
OC	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=GIR; TISSUE=Liver;			
RA	Souza S.C., Wang X., Lobo R.B., Kopchick J.J.;			
RL	Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: This is a receptor for pituitary gland growth hormone.			
CC	-!- SUBUNIT: Homodimer (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 1.			
CC	-!- SIMILARITY: Contains 1 fibronectin type III domain.			
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CC	EMBL; X70041; CAA49635.1; -.			
DR	HSNP; P10912; IA22.			
DR	InterPro; IPR002996; CR1A.			
DR	InterPro; IPR003961; FN_III.			
DR	InterPro; IPR003528; Hemtopoptn_L_Fl.			
DR	Pfam; PF00041; fn3; 1.			
DR	SMART; SM00060; FN3; 1.			
DR	PROSITE; PS01352; HEMATOPO REC_L_Fl; 1.			
KW	Receptor; Transmembrane; Glycoprotein; Signal.			
FT	SIGNAL	1	18	POTENTIAL.
FT	CHAIN	19	634	GROWTH HORMONE RECEPTOR.
FT	DOMAIN	19	260	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	261	284	POTENTIAL
FT	DOMAIN	285	634	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	141	248	FIBRONECTIN TYPE-III.
FT	DISULFID	56	66	BY SIMILARITY.
FT	DISULFID	97	108	BY SIMILARITY.
FT	DISULFID	122	136	BY SIMILARITY.
FT	CARBOHYD	46	46	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	73	73	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	111	111	N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 634 AA; 70979 MW; 91955A28296CDB2E CRC64;

Query Match 100.0%; Score 55; DB 1; Length 634;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 336 DSWVEFIELD 345

RESULT 2
GHR_SHEEP
ID GHR_SHEEP STANDARD; PRT; 634 AA.
AC Q28575;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
DE GHR.
GN Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91099608; PubMed=1980117;
RA Adams T.E., Baker L., Fiddes R.J., Brandon M.R.;
RT "The sheep growth hormone receptor: molecular cloning and ontogeny of
RT mRNA expression in the liver."
RL Mol. Cell. Endocrinol. 73:135-145(1990).
CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.
CC -!- SUBUNIT: Homodimer (by similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC -!- SIMILARITY: Subfamily 1.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
DR EMBL; M82912; AAA73171.1; .
DR PIR; S33339; S33339.
DR HSP; P10912; 1AXI.
DR InterPro; IPR002896; CRIA.
DR InterPro; IPR003961; FN.III.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPOI_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 634 GROWTH HORMONE RECEPTOR.
FT DOMAIN 19 260 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 261 284 POTENTIAL.
FT DOMAIN 285 634 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 141 248 FIBRONECTIN TYPE-III.
FT DISULFID 56 66 BY SIMILARITY.
FT DISULFID 97 108 BY SIMILARITY.
FT DISULFID 122 136 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 634 AA; 70844 MW; PFD28B9C23BC1496 CRC64;

Query Match 100.0%; Score 55; DB 1; Length 634;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 336 DSWVEFIELD 345

RESULT 3
GHR_HUMAN
ID GHR_HUMAN STANDARD; PRT; 638 AA.
AC P10912;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
DE GHR.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=88065896; PubMed=2825030;
RA Leung D.W., Spencer S.A., Cachianes G., Hammonds R.G., Collins C.,
RA Hezel W.J., Barnard R., Waters M.J., Wood W.I.;
RT "Growth hormone receptor and serum binding protein: purification,
RT cloning and expression."
RL Nature 330:537-543(1987).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT LEU-544.
RX MEDLINE=90046742; PubMed=2813379;
RA Godowski P.J., Leung D.W., Meacham L.R., Galgani J.P., Hellmiss R.,
RA Keret R., Rowein P.S., Parks J.S., Laron Z., Wood W.I.;
RT "Characterization of the human growth hormone receptor gene and
RT demonstration of a partial gene deletion in two patients with Laron-
RT type dwarfism."
RL Proc. Natl. Acad. Sci. U.S.A. 86:8083-8087(1989).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=90153957; PubMed=2406245;
RA Fuh G., Mulkerin M.G., Bass S., McFarland N., Brochier M.,
RA Bourrel J.H., Light D.R., Wells J.A.;
RT "The human growth hormone receptor. Secretion from Escherichia coli
RT and disulfide bonding pattern of the extracellular binding domain."
RL J. Biol. Chem. 265:3111-3115(1990).
RN [4]
RP VARIANT LARON DWARFISM SER-114.
RX MEDLINE=89384829; PubMed=2779634;
RA Anselm S., Duquesnoy P., Attree O., Novelli G., Boushina S.,
RA Postelvinay M.-C., Goossens M.;
RT "Laron dwarfism and mutations of the growth hormone-receptor gene."
RL New Engl. J. Med. 321:989-995(1989).
RN [5]
RP VARIANTS LARON DWARFISM.
RX MEDLINE=93278381; PubMed=8504296;
RA Anselm S., Duquesnoy P., Duriez B., Dastot F., Sorbier M.-L.,
RA Valleix S., Goossens M.;
RT "Spectrum of growth hormone receptor mutations and associated
RT haplotypes in Laron syndrome."
RL Hum. Mol. Genet. 2:355-359(1993).
RN [6]
RP VARIANT LARON DWARFISM HIS-170.
RX MEDLINE=94185645; PubMed=8137822;

```

RA Dusquesnoy P., Sobrier M.-L., Duriez B., Dastot F., Buchanan C.R.,  
 RA Savage M.O., Preece M.A., Craescu C.T., Blouquit Y., Goossens M.,  
 RA Amelém S.;  
 RA "A single amino acid substitution in the exoplasmic domain of the  
 RT human growth hormone (GH) receptor confers familial GH resistance  
 RT (Laron syndrome) with positive GH-binding activity by abolishing  
 RT receptor homodimerization.";  
 RL EMBO J. 13:1386-1395(1994).  
 RN [7]  
 RP VARIANTS IDIOPATHIC SHORT STATURE LYS-62; CYS-179 AND ASP-242.  
 RX MEDLINE=96013502; PubMed=7565946;  
 RA Goddard A.D., Covello R., Luoh S.-M., Clarkson T., Attie K.M.,  
 RA Gesundheit N., Rundle A.C., Wells J.A., Carlsson L.M.S.;  
 RA "Mutations of the growth hormone receptor in children with idiopathic  
 RT short stature.";  
 RL New Engl. J. Med. 333:1093-1098(1995).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 19-256.  
 RX MEDLINE=92196577; PubMed=1549776;  
 RA de Vos A.M., Ultsch M., Kossiakoff A.A.;  
 RA "Human growth hormone and extracellular domain of its receptor:  
 RT crystal structure of the complex.";  
 RL Science 255:306-312(1992).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 19-256.  
 RX MEDLINE=97113023; PubMed=8943276;  
 RA Sundstroem M., Lundqvist T., Roedin J., Giebel L.B., Milligan D.,  
 RA Norstedt G.;  
 RT "Crystal structure of an antagonist mutant of human growth hormone,  
 RT G120R, in complex with its receptor at 2.9-A resolution.";  
 RL J. Biol. Chem. 271:32197-32203(1996).  
 RN [10]  
 RP VARIANTS HIS-179; HIS-229; PHE-440; THR-495; LEU-544 AND THR-579.  
 RX MEDLINE=99318093; PubMed=10391209;  
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,  
 RA Lander E.S.;  
 RA "Characterization of single-nucleotide polymorphisms in coding regions  
 RT of human genes.";  
 RL Nat. Genet. 22:231-238(1999).  
 RN [11]  
 RP ERRATUM.  
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,  
 RA Lander E.S.;  
 RL Nat. Genet. 23:373-373(1999).  
 CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.  
 CC -!- SUBUNIT: Homodimer.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- DISEASE: Defects in GHR are a cause of Laron dwarfism  
 CC [MIM:262500]; also known as pituitary dwarfism II (Laron-type  
 CC pituitary dwarfism or Laron syndrome [LS]).  
 CC -!- DISEASE: Defects in GHR are a cause of idiopathic short stature  
 CC [MIM:600946].  
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC Subfamily 1.  
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.  
 CC -----  
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 CC -----  
 DR EMBL; X06562; CAA29808.1; --  
 DR EMBL; M28466; AAA52555.1; --  
 DR EMBL; M28458; AAA52555.1; JOINED.  
 DR EMBL; M28459; AAA52555.1; JOINED.  
 DR EMBL; M28460; AAA52555.1; JOINED.

DR EMBL; M28461; AAA52555.1; JOINED.  
 DR EMBL; M28462; AAA52555.1; JOINED.  
 DR EMBL; M28463; AAA52555.1; JOINED.  
 DR EMBL; M28464; AAA52555.1; JOINED.  
 DR EMBL; M28465; AAA52555.1; JOINED.  
 DR PIR; A33991; A33991.  
 DR PDB; 3HRH; 30-APR-94.  
 DR PDB; 1HWG; 19-NOV-97.  
 DR PDB; 1AXI; 28-JAN-98.  
 DR PDB; 1A22; 29-APR-98.  
 DR PDB; 1KF9; 20-NOV-02.  
 DR Genew; HGNC:4263; GHR.  
 DR MIM; 600946; --  
 DR MIM; 262500; --  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0004903; F:growth hormone receptor activity; TAS.  
 DR GO; GO:0007150; P:growth pattern; TAS.  
 DR GO; GO:0001501; P:skeletal development; TAS.  
 DR InterPro; IPR002996; CR1A.  
 DR InterPro; IPR003961; FN\_III.  
 DR Pfam; PF00041; fn3; 1.  
 DR SMART; SM00060; FN3; 1.  
 DR PROSITE; PS01352; HEMATOPO REC\_L\_F1; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure;  
 KW Dwarfism; Polymorphism; Disease mutation.  
 FT SIGNAL 1 18  
 FT CHAIN 19 638  
 FT DOMAIN 19 264  
 FT TRANSMEM 265 288  
 FT DOMAIN 289 638  
 FT DOMAIN 145 252  
 FT DISULFID 56 66  
 FT DISULFID 101 112  
 FT DISULFID 126 140  
 FT CARBOHYD 46 46  
 FT CARBOHYD 115 115  
 FT CARBOHYD 156 156  
 FT CARBOHYD 161 161  
 FT CARBOHYD 200 200  
 FT VARIANT 62 62  
 FT VARIANT 89 89  
 FT VARIANT 114 114  
 FT VARIANT 143 143  
 FT VARIANT 162 162  
 FT VARIANT 170 170  
 FT VARIANT 179 179  
 FT VARIANT 179 179  
 FT VARIANT 229 229  
 FT VARIANT 229 229  
 FT VARIANT 242 242  
 FT VARIANT 440 440  
 FT VARIANT 495 495  
 FT VARIANT 544 544  
 FT  
 FT N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT E -> K (in idiopathic short stature).  
 FT /FTId=VAR\_002708  
 FT R -> K (in Laron dwarfism).  
 FT /FTId=VAR\_002709.  
 FT F -> S (in Laron dwarfism).  
 FT /FTId=VAR\_002710.  
 FT V -> A (in Laron dwarfism).  
 FT /FTId=VAR\_002711.  
 FT V -> D (in Laron dwarfism).  
 FT /FTId=VAR\_002712.  
 FT D -> H (in Laron dwarfism; abolish  
 FT receptor homodimerization).  
 FT /FTId=VAR\_002713.  
 FT R -> C (in Laron dwarfism and idiopathic  
 FT short stature).  
 FT /FTId=VAR\_002714.  
 FT R -> H (in dbSNP:6181).  
 FT /FTId=VAR\_013937.  
 FT R -> G (in Laron dwarfism).  
 FT /FTId=VAR\_002715.  
 FT R -> H (in dbSNP:6177).  
 FT /FTId=VAR\_013938.  
 FT E -> D (in idiopathic short stature).  
 FT /FTId=VAR\_002716.  
 FT C -> F (in dbSNP:6182).  
 FT /FTId=VAR\_013939.  
 FT P -> T (in dbSNP:6183).  
 FT /FTId=VAR\_013940.  
 FT I -> L (in dbSNP:6180).  
 FT /FTId=VAR\_013941.

Query Match

100.0%; Score 55; DB 1; Length 638;





GHR\_RABIT STANDARD; PRT; 638 AA.

AC P19941;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).  
 DE protein).  
 GN GHR.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
 RX MEDLINE=8805896; PubMed=2825030;  
 RA Leung D.W., Spencer S.A., Cachianes G., Hammonds R.G., Collins C.,  
 RA Henzel W.J., Barnard R., Waters M.J., Wood W.I.;  
 RT "Growth hormone receptor and serum binding protein: purification,  
 RT cloning and expression.";  
 RL Nature 330:537-543 (1987).  
 CC -1- FUNCTION: This is a receptor for pituitary gland growth hormone.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.  
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 CC  
 DR EMBL; AF015252; AAB67613.1; -.  
 DR PIR; S08544; B28176.  
 DR HSP; P10912; I22.  
 DR InterPro; IPR002996; CR1A.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003528; Hemopoptn\_L\_Fl.  
 DR Pfam; PF00041; fn3; 1.  
 DR SMART; SM00060; FN3; 1.  
 DR PROSITE; PS01352; HEMATOPO\_REC\_L\_Fl; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 19 638 GROWTH HORMONE RECEPTOR.  
 FT DOMAIN 19 264 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 265 288 POTENTIAL.  
 FT DOMAIN 289 638 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 145 252 FIBRONECTIN TYPE-III.  
 FT DISULFID 56 66 BY SIMILARITY.  
 FT DISULFID 101 112 BY SIMILARITY.  
 FT DISULFID 126 140 BY SIMILARITY.  
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 638 AA; 71076 MW; B05CCE1D7294624C CRC64;  
 Query Match 100.0%; Score 55; DB 1; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSWVEFIELD 10  
 Db 340 DSWVEFIELD 349

RESULT 7  
 GHR\_RAT

GHR\_RAT STANDARD; PRT; 638 AA.

P16310;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).  
 DE protein).  
 GN GHR.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89255563; PubMed=2722883;  
 RA Mathews L.S., Enberg B., Norsted G.;  
 RT "Regulation of rat growth hormone receptor gene expression.";  
 RL J. Biol. Chem. 264:9905-9910 (1989).  
 CC -1- FUNCTION: This is a receptor for pituitary gland growth hormone.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC -1- SIMILARITY: Contains 1 fibronectin type III domain.  
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 CC  
 DR EMBL; J04811; AAA41219.1; -.  
 DR PIR; A32985; A33505.  
 DR HSP; P10912; I22.  
 DR InterPro; IPR002996; CR1A.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003528; Hemopoptn\_L\_Fl.  
 DR Pfam; PF00041; fn3; 1.  
 DR SMART; SM00060; FN3; 1.  
 DR PROSITE; PS01352; HEMATOPO\_REC\_L\_Fl; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 638 GROWTH HORMONE RECEPTOR.  
 FT DOMAIN 19 265 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 266 289 POTENTIAL.  
 FT DOMAIN 290 638 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 145 252 FIBRONECTIN TYPE-III.  
 FT DISULFID 56 66 BY SIMILARITY.  
 FT DISULFID 101 112 BY SIMILARITY.  
 FT DISULFID 126 140 BY SIMILARITY.  
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 200 200 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 638 AA; 71236 MW; 0D8E9AF759A21A3B CRC64;  
 Query Match 100.0%; Score 55; DB 1; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 0.014;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DSWVEFIELD 10  
 Db 341 DSWVEFIELD 350

```

RESULT 8
GHR_MOUSE
ID GHR_MOUSE STANDARD; PRT; 650 AA.
AC P16882; P16590; Q9R264;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (GH binding protein)
DE (GHRP) (Serum binding protein).
GN GHR.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=9295449; PubMed=2739661;
RT Smith W.C., Kuniyoshi J., Talamantes F.;
RT "Mouse serum growth hormone (GH) binding protein has GH receptor
RT extracellular and substituted transmembrane domains.";
RL Mol. Endocrinol. 3:984-990(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX STRAIN=Swiss Webster, and DBA/2J;
RX MEDLINE=9367316; PubMed=10425445;
RA Moffat J.G., Edens A., Talamantes F.;
RA "Structure and expression of the mouse growth hormone receptor/growth
RT hormone binding protein gene.";
RL J. Mol. Endocrinol. 23:333-44(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX STRAIN=Swiss Webster, and DBA/2J;
RX MEDLINE=95080157; PubMed=7988474;
RA Edens A., Southard J.N., Talamantes F.;
RA "Mouse growth hormone receptor/binding protein and growth hormone
RT receptor transcripts are produced from a single gene by alternative
RT splicing.";
RL Endocrinology 135:2802-2805(1994).
RN [4]
RP SEQUENCE OF 156-650 FROM N.A. (ISOFORM 1).
RX STRAIN=C57BL/6;
RX MEDLINE=95201642; PubMed=7894338;
RA Zhou Y., He L., Kopchick J.J.;
RA "An exon encoding the mouse growth hormone binding protein (mGHRP)
RT carboxy terminus is located between exon 7 and 8 of the mouse growth
RT hormone receptor gene.";
RL Receptor 4:223-227(1994).
RN [5]
RP REVISIONS.
RA Zhou Y., He L., Kopchick J.J.;
RA Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 25-41.
RX MEDLINE=88288223; PubMed=3398846;
RA Smith W.C., Colosi P., Talamantes F.;
RA "Isolation of two molecular weight variants of the mouse growth
RT hormone receptor.";
RL Mol. Endocrinol. 2:108-116(1988).
RN [7]
RP FUNCTION: Isoform 1 is a receptor for pituitary gland growth
CC hormone. Isoform 2 is a serum growth hormone binding protein that
CC may play an important role in regulating the effective serum
CC concentration of gh.
CC
CC -1- SUBUNIT: Isoform 1 is a homodimer.
CC
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC Secreted (isoform 2).
CC
CC -1- ALTERNATIVE PRODUCTS:
CC Name=1; Synonyms=HWM GHR;
CC IsoId=P16882-1; Sequence=Displayed;
CC Name=2; Synonyms=LWM GHR;
CC IsoId=P16882-2; Sequence=VSP_001716, VSP_001717;
CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.

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CC Subfamily 1.
CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
CC
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CC
CC EMBL; M33324; AAA37690.1; ALT SEQ.
DR EMBL; M31680; AAA37689.1; ALT SEQ.
DR EMBL; AF120489; AAD32556.1; JOINED.
DR EMBL; AF120481; AAD32556.1; JOINED.
DR EMBL; AF120482; AAD32556.1; JOINED.
DR EMBL; AF120483; AAD32556.1; JOINED.
DR EMBL; AF120484; AAD32556.1; JOINED.
DR EMBL; AF120485; AAD32556.1; JOINED.
DR EMBL; AF120486; AAD32556.1; JOINED.
DR EMBL; AF120487; AAD32556.1; JOINED.
DR EMBL; AF120488; AAD32556.1; JOINED.
DR EMBL; AF120487; AAD32555.1; JOINED.
DR EMBL; AF120481; AAD32555.1; JOINED.
DR EMBL; AF120482; AAD32555.1; JOINED.
DR EMBL; AF120483; AAD32555.1; JOINED.
DR EMBL; AF120484; AAD32555.1; JOINED.
DR EMBL; AF120485; AAD32555.1; JOINED.
DR EMBL; AF120486; AAD32555.1; JOINED.
DR EMBL; U49266; AAK62802.1; JOINED.
DR EMBL; U49268; AAK62802.1; JOINED.
DR EMBL; U43933; AAK62802.1; JOINED.
DR HSP; P10912; IAA2.
DR MGD; MGI:95708; Ghr.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hemtopoptn_L_Fl.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO RECL Fl; 1.
DR Receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
KW SIGNAL
FT CHAIN 1 24
FT DOMAIN 25 273
FT TRANSMEM 274 297
FT DOMAIN 298 650
FT DOMAIN 153 260
FT DISULFID 56 66
FT DISULFID 109 120
FT DISULFID 134 148
FT CARBOHYD 123 123
FT CARBOHYD 164 164
FT CARBOHYD 169 169
FT CARBOHYD 208 208
FT VARSPLIC 271 296
FT
FT VARSPLIC 297 650
FT
FT CONFLICT 25 25
FT CONFLICT 162 162
FT CONFLICT 325 325
FT CONFLICT 423 423
SQ SEQUENCE 650 AA; 72783 MW; 95653380CAF0B931 CRC64;
Query Match 100.0%; Score 55; DB 1; Length 650;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DSWVERIELD 10
DB 349 DSWVERIELD 358

```

## RESULT 9

GHR\_CHICK STANDARD; PRT; 608 AA.

AC Q02092; (Rel. 26, Created)

DT 01-JUN-1993 (Rel. 26, Last sequence update)

DT 01-JUN-1993 (Rel. 26, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).

DE DE protein).

GN GHR.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianinae; Gallus.

OC NCBI\_TaxID=9031;

OX [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Liver;

RX MEDLINE=91243665; PubMed=2036984;

RA Burnside J., Liou S.S., Cogburn L.A.;

RT "Molecular cloning of the chicken growth hormone receptor complementary deoxyribonucleic acid: mutation of the gene in sex-linked dwarf chickens."

RT Endocrinology 128:3183-3192(1991).

CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.

CC -!- SUBUNIT: Homodimer.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Broad specificity.

CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 1.

CC -!- SIMILARITY: Contains 1 fibronectin type III domain.

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CC EMBL: M74057; AAA48781.1; -.

DR F1R; S32823; S32823.

DR HSSP; P10912; IAXI.

DR InterPro; IPR002996; CRI1A.

DR InterPro; IPR008957; FN III-like.

DR InterPro; IPR003961; FN III.

DR InterPro; IPR003528; Hemoptoptn\_L\_F1.

DR Pfam; PF00041; fn3; 1.

DR SMART; SM00060; FN3; 1.

DR PROSITE; PS01352; HEMATOPO REC L\_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 16 POTENTIAL.

FT CHAIN 17 608 GROWTH HORMONE RECEPTOR.

FT DOMAIN 17 237 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 238 261 POTENTIAL.

FT DOMAIN 262 608 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 117 223 FIBRONECTIN TYPE-III.

FT DISULFID 34 44 BY SIMILARITY.

FT DISULFID 72 83 BY SIMILARITY.

FT DISULFID 97 111 BY SIMILARITY.

FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 608 AA; 68572 MW; D71AD7B6C62528DC CRC64;

Query Match 89.1%; Score 49; DB 1; Length 608;

Best Local Similarity 90.0%; Pred. No. 0.18;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10

DB 313 DLWVEFIELD 322

## RESULT 10

GHR\_COLLI STANDARD; PRT; 611 AA.

AC Q90375;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Growth hormone receptor precursor (GH receptor) (Serum binding protein).

DE DE protein).

GN GHR.

OS Columba livia (Domestic pigeon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.

OC NCBI\_TaxID=8932;

OX [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Liver;

RA Cheng C.H.K., Shaw P.C., Tsim K.W.K., Lau K.F.;

RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.

CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors. Subfamily 1.

CC -!- SIMILARITY: Contains 1 fibronectin type III domain.

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CC EMBL: U20353; AAA84745.1; -.

DR HSSP; P10912; IAXI.

DR InterPro; IPR002996; CRI1A.

DR InterPro; IPR008957; FN III-like.

DR InterPro; IPR003961; FN III.

DR InterPro; IPR003528; Hemoptoptn\_L\_F1.

DR Pfam; PF00041; fn3; 1.

DR SMART; SM00060; FN3; 1.

DR PROSITE; PS01352; HEMATOPO REC L\_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal.

FT SIGNAL 1 20 POTENTIAL.

FT CHAIN 21 611 GROWTH HORMONE RECEPTOR.

FT DOMAIN 21 240 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 241 264 POTENTIAL.

FT DOMAIN 265 611 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 119 226 FIBRONECTIN TYPE-III.

FT DISULFID 34 44 BY SIMILARITY.

FT DISULFID 75 86 BY SIMILARITY.

FT DISULFID 100 114 BY SIMILARITY.

FT CARBOHYD 16 16 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 611 AA; 68851 MW; C48750BF9E4EBDA CRC64;

Query Match 89.1%; Score 49; DB 1; Length 611;

Best Local Similarity 90.0%; Pred. No. 0.18;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10

DB 316 DLWVEFIELD 325

RESULT 11

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RPOC_PSEPU
ID _RPOC_PSEPU STANDARD; PRT; 1409 AA.
AC P19176;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (transcriptase
DE beta' chain) (RNA polymerase beta' subunit).
GN RPOC.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
CX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RA Danilovich A.V., Borodin A.M., Allikmets R.L., Rostapshov V.M.,
RA Chernov I.P., Azhikina T.I., Monastyrskaya G.S., Sverdlov E.D.;
RT "Nucleotide sequence of the rpoC gene coding for the beta'-subunit of
RT RNA polymerase in Pseudomonas putida.";
RL Dokl. Biochem. 303:241-245 (1988).
RN [2]
RP SEQUENCE OF 1-497 FROM N.A.
RX MEDLINE=89117617; PubMed=3219133;
RA Borodin A.M., Danilovich A.V., Chernov I.P., Azhikina T.L.,
RA Rostapshov V.M., Monastyrskaya G.S.;
RT "Genes coding for RNA polymerase in bacteria. III. The use of
RT modified Sanger's method for sequencing the C-terminal region of rpoB
RT gene, N-terminal region of rpoC gene and intercistron region of rpoB
RT polymerase in Pseudomonas putida.";
RL Bioorg. Khim. 14:1179-1182 (1988).
CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC of DNA into RNA using the four ribonucleoside triphosphates as
CC substrates.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}[N].
CC -!- SUBUNIT: The enzyme consists of the sigma chain and the core
CC enzyme which is composed of 2 alpha chains, 1 beta chain, and 1
CC beta' chain.
CC -!- SIMILARITY: Belongs to the RNA polymerase beta' chain family.
CC
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CC
CC -----
CC EMBL; X16538; CAA34538.1; -.
CC EMBL; M38319; AAA25987.1; -.
CC PIR; JN0420; JN0420.
CC HSSP; Q9KWU6; 1HQW.
CC InterPro; IPR000722; RNA_pol_A.
CC InterPro; IPR007080; RNA_pol_Rpb1_1.
CC InterPro; IPR007066; RNA_pol_Rpb1_3.
CC InterPro; IPR007083; RNA_pol_Rpb1_4.
CC InterPro; IPR007081; RNA_pol_Rpb1_5.
CC InterPro; IPR006592; RNA_pol_N_.
CC Pfam; PF04997; RNA_pol_Rpb1_1.
CC Pfam; PF00623; RNA_pol_Rpb1_2.
CC Pfam; PF04983; RNA_pol_Rpb1_3.
CC Pfam; PF05000; RNA_pol_Rpb1_4.
CC Pfam; PF04998; RNA_pol_Rpb1_5.
CC SMART; SM00663; RPOA_N; 1.
KW Transferase; DNA-directed RNA polymerase; Transcription.
FT CONFLICT 2 2 P -> L (IN REF. 2).
FT CONFLICT 17 17 N -> I (IN REF. 2).
FT CONFLICT 89 89 L -> V (IN REF. 2).
FT CONFLICT 203 203 I -> T (IN REF. 2).
FT CONFLICT 328 328 I -> T (IN REF. 2).
FT CONFLICT 335 335 L -> S (IN REF. 2).
FT CONFLICT 348 348 L -> R (IN REF. 2).
FT CONFLICT 482 482 P -> L (IN REF. 2).
FT

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FT CONFLICT 484 484 T -> I (IN REF. 2).
SQ SEQUENCE 1409 AA; 154544 MW; C5662109D3BE3D81 CRC64;

Query Match 76.4%; Score 42; DB 1; Length 1409;
Best Local Similarity 70.0%; Pred. No. 8.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
DB 877 EQWVEFIELDN 886

RESULT 12
SSP2_BOMMO STANDARD; PRT; 704 AA.
AC P20613;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Sex-specific storage-protein 2 precursor.
GN SP2.
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
CX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89201839; PubMed=2544581;
RA Fujii T., Sakurai H., Izumi S., Tomino S.;
RT "Structure of the gene for the arylphorin-type storage protein SP 2
RT of Bombyx mori.";
RL J. Biol. Chem. 264:11020-11025 (1989).
CC -!- FUNCTION: Larval storage protein (ISP) which may serve as a store
CC of amino acids for synthesis of adult proteins.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Fat body.
CC -!- SIMILARITY: TO ARYLPHORINS AND TO ARTHROPOD HEMOCYANINS.
CC
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CC
CC -----
CC EMBL; M24370; AAA27848.1; -.
CC EMBL; M24371; AAA27848.1; JOINED.
CC PIR; A34287; A34287.
CC HSSP; P04253; 1OXY.
CC InterPro; IPR008922; Di-copper centre.
CC InterPro; IPR000896; Hemocyanin.
CC InterPro; IPR005203; hemocyanin_C.
CC InterPro; IPR005204; hemocyanin_N.
CC InterPro; IPR007110; Ig-like.
CC Pfam; PF00372; hemocyanin_1.
CC Pfam; PF03723; hemocyanin_C; 1.
CC Pfam; PF03722; hemocyanin_N; 1.
CC PRINTS; PR00187; HAEMOCYANIN.
CC PROSITE; PS00209; HEMOCYANIN_1; 1.
CC PROSITE; PS00210; HEMOCYANIN_2; 1.
CC SIGNAL; Storage protein; Glycoprotein.
FT SIGNAL 1 16
FT CHAIN 17 704 SEX-SPECIFIC STORAGE-PROTEIN 2.
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 681 681 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 704 AA; 83466 MW; 365E7DFB707137EB CRC64;

Query Match 74.5%; Score 41; DB 1; Length 704;
Best Local Similarity 60.0%; Pred. No. 6.4;

```

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVERFIELD 10  
Db 544 DNMMKFELD 553

RESULT 13  
VGR3 MOUSE  
ID\_VGR3 MOUSE STANDARD; PRT; 1363 AA.

AC P35917;  
DT 01-JUN-1994 (Rel. 29, last sequence update)  
DT 01-JUN-1994 (Rel. 29, last sequence update)  
DT 10-OCT-2003 (Rel. 42, last annotation update)  
DE Vascular endothelial growth factor receptor 3 precursor (EC 2.7.1.112)  
DE (VEGFR-3) (Tyrosine-protein kinase receptor FLT4).  
GN FLT4 OR FLT-4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=93330572; PubMed=8393164;  
RA Finnerty H., Kelleher K., Morris G.E., Bean K., Merberg D.M.,  
RA Kriz R., Morris J.C., Sookdeo H., Turner K.J., Wood C.R.;  
RT "Molecular cloning of murine FLT and FLT4";  
RL Oncogene 8:2293-2298(1993).  
CC -1- FUNCTION: RECEPTOR FOR VEGF-C. HAS A TYROSINE-PROTEIN KINASE  
CC ACTIVITY.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
CC tyrosine phosphate.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ADULT LUNG AND LIVER, AND IN  
CC FETAL LIVER, BRAIN, INTESTINE AND PLACENTA.  
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases.  
CC CSF-1/PDGF receptor subfamily.  
CC -1- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.

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EMBL; L07296; AAA00077.1; -.  
PIR; I58375; I58375.  
DR HSSP; P11362; 1FGK.  
MGD; MGI:95561; Flt4.  
GO; GO:0005515; F;protein binding; IPI.  
InterPro; IPR007110; Ig-like.  
InterPro; IPR003598; Ig\_c2.  
InterPro; IPR000719; Prot kinase.  
InterPro; IPR001824; RecepttyrkinsIII.  
InterPro; IPR001245; Tyr\_kinase.  
InterPro; IPR008266; Tyr\_kinase\_AS.  
Pfam; PF00047; Ig; 5.  
Pfam; PF00069; pkinase; 1.  
ProDom; PD000001; Prot kinase; 2.  
SMART; SM00408; IGC2; 2.  
SMART; SM00219; TyfKc; 1.  
PROSITE; PS00835; IG\_LIKE; 5.  
PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
PROSITE; PS50011; PROTEIN KINASE DOM; 1.  
PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
PROSITE; PS00240; RECEPTOR\_TYR\_KIN\_III; 1.  
Transferase; Tyrosine-protein Kinase; Phosphorylation; ATP-binding;  
KW Receptor; Transmembrane; Signal; Immunoglobulin domain; Repeat;  
KW Glycoprotein.  
FT SIGNAL 1 24 POTENTIAL.

FT CHAIN 25 1363 VASCULAR ENDOTHELIAL GROWTH FACTOR  
FT RECEPTOR 3.  
FT EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM  
FT DOMAIN 25 775  
FT TRANSMEM 776 797  
FT DOMAIN 798 1363 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 44 118 IG-LIKE C2-TYPE 1.  
FT DOMAIN 151 213 IG-LIKE C2-TYPE 2.  
FT DOMAIN 230 326 IG-LIKE C2-TYPE 3.  
FT DOMAIN 331 415 IG-LIKE C2-TYPE 4.  
FT DOMAIN 422 552 IG-LIKE C2-TYPE 5.  
FT DOMAIN 555 671 IG-LIKE C2-TYPE 6.  
FT DOMAIN 678 764 IG-LIKE C2-TYPE 7.  
FT DOMAIN 845 1173 PROTEIN KINASE.  
FT NP\_BIND 851 859 ATP (BY SIMILARITY).  
FT BINDING 879 879 ATP (BY SIMILARITY).  
FT ACT\_SITE 1037 1037 BY SIMILARITY.  
FT DISULFID 51 111 POTENTIAL.  
FT DISULFID 158 206 POTENTIAL.  
FT DISULFID 252 310 POTENTIAL.  
FT DISULFID 445 534 POTENTIAL.  
FT DISULFID 578 653 POTENTIAL.  
FT DISULFID 699 751 POTENTIAL.  
FT MOD\_RES 1068 1068 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT CARBOHYD 33 33 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 104 104 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 166 166 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 251 251 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 299 299 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 411 411 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 515 515 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 527 527 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 582 582 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 594 594 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 683 683 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 690 690 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 758 758 N-LINKED (GLCNAC...) (POTENTIAL).  
SQ SEQUENCE 1363 AA; 153015 MW; F1BF8A2BDEF99BE9 CRC64;

Query Match 72.7%; Score 40; DB 1; Length 1363;  
Best Local Similarity 75.0%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DSWVERIE 8  
Db 505 DSWTEFVE 512

RESULT 14  
SR09 MAIZE  
ID\_SR09 MAIZE STANDARD; PRT; 103 AA.  
AC O04438;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, last sequence update)  
DT 16-OCT-2001 (Rel. 40, last annotation update)  
DE Signal recognition particle 9 kDa protein (SRP9).  
GN SRP9.  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. W64A2;  
RA Bui N., Wolff N., Strub K.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Signal-recognition-particle assembly has a crucial role  
CC in targeting secretory proteins to the rough endoplasmic reticulum  
CC membrane. SRP9 together with SRP14 and the Alu portion of the SRP  
CC RNA, constitutes the elongation arrest domain of SRP. The complex  
CC of SRP9 and SRP14 is required for SRP RNA binding (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: Belongs to the SRP9 family.

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CC -----
DR EMBL; Y10117; CAA71203.1; -.
DR PIR; T03951; T03951.
DR HSP; P49962; 1914.
DR InterPro; IPR008832; SRP9.
DR InterPro; IPR009018; SRP9/14.
DR Pfam; PF05486; SRP9; 1.
KW Signal recognition particle; RNA-binding.
SQ SEQUENCE 103 AA; 12077 MW; B6EFAA9DA77C13BE CRC64;
Query Match 69.1%; Score 38; DB 1; Length 103;
Best Local Similarity 75.0%; Pred. No. 3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 DSWVEFTE 8
Db |||||:|
5 DSWEEFVE 12
RESULT 15
MURB SHEON STANDARD; PRT; 341 AA.
ID MURB SHEON STANDARD; PRT; 341 AA.
AC Q8EK85;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE UDP-N-acetylpyruvoylglucosamine reductase (EC 1.1.1.158) (UDP-N-
DE acetylmutamate dehydrogenase).
DE MURB OR S00213.
GN Shewanella oneidensis.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
RA Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
RA Vanathavan J., Weidman J., Imbraim M., Lee K., Berry K., Lee C.,
RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Nealon K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
CC -!- FUNCTION: Cell wall formation (By similarity).
CC -!- CATALYTIC ACTIVITY: UDP-N-acetylmuramate + NADP(+) = UDP-N-
CC acetyl-3-O-(1-carboxyvinyl)-D-glucosamine + NADPH.
CC -!- COFACTOR: FAD (By similarity).
CC -!- PATHWAY: Peptidoglycan biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: Belongs to the murB family.
CC -----
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CC -----
DR EMBL; AE015471; AAN53298.1; -.

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DR TIGR; S00213; -.
DR HAMAP; MF 00037; -.
DR InterPro; IPR003170; MurB.
DR InterPro; IPR006094; Oxid_FAD_bind.
DR Pfam; PF01565; FAD_binding_4; 1.
DR TIGRFAMS; TIGR00179; murB; 1.
DR Oxidoreductase; NADP; Flavoprotein; FAD; Cell wall; Cell division;
KW Peptidoglycan synthesis; Complete proteome.
SQ SEQUENCE 341 AA; 37278 MW; FAE630BA722A3073 CRC64;
Query Match 67.3%; Score 37; DB 1; Length 341;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 3 WVEFIELD 10
Db |||||:|
137 WVEYLDLD 144
Search completed: June 9, 2004, 15:49:05
Job time : 7.2973 secs

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 9, 2004, 15:43:00 ; Search time 33.5135 Seconds  
(without alignments)  
94.147 Million cell updates/sec

Title: US-09-660-302D-3  
Perfect score: 55  
Sequence: 1 DSWVEFIELD 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTEMBL 25.\*

1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_ivirius.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	55	100.0	101	6 Q863N9	arctonyx co
2	55	100.0	105	6 Q863Q6	lontra cana
3	55	100.0	105	6 Q863P4	eira barbar
4	55	100.0	106	6 Q863Q3	lutra lutra
5	55	100.0	106	6 Q863Q2	lutra macul
6	55	100.0	107	6 Q863Q9	aconyx capen
7	55	100.0	107	6 Q863Q8	amblyonx ci
8	55	100.0	107	6 Q863Q7	enhydra lut
9	55	100.0	107	6 Q863Q5	lontra feli
10	55	100.0	107	6 Q863Q4	lontra long
11	55	100.0	107	6 Q863Q1	pteronura b
12	55	100.0	107	6 Q863Q0	mustela erm
13	55	100.0	107	6 Q863P9	mustela fire
14	55	100.0	107	6 Q863P8	mustela vis
15	55	100.0	107	6 Q863P7	martes amer
16	55	100.0	107	6 Q863P6	martes penn

17	55	100.0	107	6 Q863P5	gulo gulo (
18	55	100.0	107	6 Q863P2	ictonyx str
19	55	100.0	107	6 Q863P1	meles meles
20	55	100.0	107	6 Q863P0	taxidea tax
21	55	100.0	107	6 Q863N8	melogale mo
22	55	100.0	107	6 Q863N7	bassariscus
23	55	100.0	107	6 Q863N6	procyon lot
24	55	100.0	130	11 Q99MY7	meriones un
25	55	100.0	233	6 Q95MM1	ochotona pr
26	55	100.0	238	11 Q924F8	perognathus
27	55	100.0	293	6 Q8MJW2	elephantulu
28	55	100.0	294	6 Q95ML9	sylvilagus
29	55	100.0	294	6 Q8MJL9	ursus ameri
30	55	100.0	295	6 Q95ML8	tupaia bela
31	55	100.0	295	11 Q80Z48	ctenomys st
32	55	100.0	296	11 Q924F4	hystrix afr
33	55	100.0	296	11 Q924F1	chinchilla
34	55	100.0	296	11 Q924E8	proechimys
35	55	100.0	296	11 Q924F2	thryonomys
36	55	100.0	296	11 Q924F3	heteroceph
37	55	100.0	296	11 Q924B9	dinomys bra
38	55	100.0	296	11 Q924F0	erethizon d
39	55	100.0	296	11 Q80Z55	aconaemys p
40	55	100.0	296	11 Q80Z54	octodon bri
41	55	100.0	296	11 Q80Z53	octodontomy
42	55	100.0	296	11 Q80Z52	spalacopus
43	55	100.0	296	11 Q80Z51	typanoctom
44	55	100.0	296	11 Q80Z49	aconaemys f
45	55	100.0	296	11 Q80Z47	

## ALIGNMENTS

## RESULT 1

Q863N9 ID Q863N9 PRELIMINARY; PRT; 101 AA.  
AC Q863N9; DT 01-JUN-2003 (TReMBLrel. 24, Created)  
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Growth hormone receptor (Fragment).  
GN GHR.  
OS Arctonyx collaris.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Melinae;  
OC Arctonyx.  
OX NCBI\_TaxID=139309;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Koepfli K.-P., Wayne R.K.;  
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in  
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";  
RL Syst. Biol. 0:0-0(2003).  
DR EMBL; AF498204; AAP19695.1; -;  
DR GO; GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
FT NON TER 1  
FT NON TER 101 101  
SQ SEQUENCE 101 AA; 11428 MW; AD696CB6E0B8D7AC CRC64;

Query Match 100.0%; Score 55; DB 6; Length 101;  
Best Local Similarity 100.0%; Pred. No. 0.01;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10  
Db 25 DSWVEFIELD 34

## RESULT 2

Q863Q6 ID Q863Q6 PRELIMINARY; PRT; 105 AA.

```

AC Q86306;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lontra canadensis (River otter) (Lontra canadensis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinidae;
OC Lontra.
OX NCBI_TaxID=76717;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL: AF498187; AAP19678.1; -.
DR GO: GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1
FT NON TER 105
SQ SEQUENCE 105 AA; 11852 MW; F07A7052451EB8E7 CRC64;

Query Match 100.0%; Score 55; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
Db 29 DSWVEFIELD 38

RESULT 3
Q863P4
ID Q863P4 PRELIMINARY; PRT; 105 AA.
AC Q863P4;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Eira barbara (Tayra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Eira.
OX NCBI_TaxID=204263;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL: AF498199; AAP19690.1; -.
DR GO: GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1
FT NON TER 105
SQ SEQUENCE 105 AA; 11879 MW; F6F6445250DB79BF CRC64;

Query Match 100.0%; Score 55; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
Db 29 DSWVEFIELD 38

RESULT 4
Q863Q3
ID Q863Q3 PRELIMINARY; PRT; 106 AA.
AC Q863Q3;

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DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lontra lutra (European river otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinidae;
OC Lontra.
OX NCBI_TaxID=9657;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL: AF498190; AAP19681.1; -.
DR GO: GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1
FT NON TER 106
SQ SEQUENCE 106 AA; 12006 MW; EFB0C6D8793AE9FF CRC64;

Query Match 100.0%; Score 55; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
Db 30 DSWVEFIELD 39

RESULT 5
Q863Q2
ID Q863Q2 PRELIMINARY; PRT; 106 AA.
AC Q863Q2;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lutra maculicollis (Spotted necked otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinidae;
OC Lutra.
OX NCBI_TaxID=76719;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL: AF498191; AAP19682.1; -.
DR GO: GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1
FT NON TER 106
SQ SEQUENCE 106 AA; 12003 MW; EFB0DDAEA24C29FF CRC64;

Query Match 100.0%; Score 55; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSWVEFIELD 10
Db 30 DSWVEFIELD 39

RESULT 6
Q863Q9
ID Q863Q9 PRELIMINARY; PRT; 107 AA.
AC Q863Q9;
DT 01-JUN-2003 (TReMBLrel. 24, Created)

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DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Anonyx capensis (Cape clawless otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Anonyx.
OX NCBI_TaxID=76722;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498184; AAP19675.1; -.
DR GO; GO:0004872; Fireceptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12101 MW; 7F3D579D3C26011B CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 7
Q863Q8 ID Q863Q8 PRELIMINARY; PRT; 107 AA.
AC Q863Q8;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Amblyonyx cinereus (Asian small-clawed otter) (Anonyx cinereus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Amblyonyx.
OX NCBI_TaxID=55043;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498185; AAP19676.1; -.
DR GO; GO:0004872; Fireceptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12121 MW; 84DD579D3C2EB8BA CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 8
Q863Q7 ID Q863Q7 PRELIMINARY; PRT; 107 AA.
AC Q863Q7;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)

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DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Euhadra lutris (Sea otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Euhadra.
OX NCBI_TaxID=34882;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498186; AAP19677.1; -.
DR GO; GO:0004872; Fireceptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12151 MW; 84DD579D3C2EA9FE CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 9
Q863Q5 ID Q863Q5 PRELIMINARY; PRT; 107 AA.
AC Q863Q5;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Lontra felina (Sea cat) (Lutra felina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Lontra.
OX NCBI_TaxID=76718;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498188; AAP19679.1; -.
DR GO; GO:0004872; Fireceptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 12180 MW; 9113E140F3C5C3BB CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 10
Q863Q4 ID Q863Q4 PRELIMINARY; PRT; 107 AA.
AC Q863Q4;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

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DE Growth hormone receptor (Fragment).
GN GHR.
OS Lontra longicaudis (Neotropical otter) (Lutra longicaudis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Lontra.
OX NCBI_TaxID=71113;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498193; AAP19684.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12166 MW; 9113E146451EA8BB CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 11
Q863Q1 ID Q863Q1 PRELIMINARY; PRT; 107 AA.
AC Q863Q1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Pteronura brasiliensis (Giant otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Lutrinae;
OC Pteronura.
OX NCBI_TaxID=9672;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498192; AAP19683.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12137 MW; 96DBCA309E7789FE CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 12
Q863Q0 ID Q863Q0 PRELIMINARY; PRT; 107 AA.
AC Q863Q0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
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GN GHR.
OS Mustela erminea (Ermine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=36723;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498193; AAP19684.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12140 MW; 96DBD146450149FE CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 13
Q863P9 ID Q863P9 PRELIMINARY; PRT; 107 AA.
AC Q863P9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Mustela frenata (Long-tailed weasel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=55048;
RN [1]
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498194; AAP19685.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 12140 MW; 96DBD146450149FE CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 14
Q863P8 ID Q863P8 PRELIMINARY; PRT; 107 AA.
AC Q863P8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
```

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OS Mustela vison (American mink).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Mustela.
OX NCBI_TaxID=9667;
RN [1];
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498195; AAP19686.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1
FT NON TER 107 107
SQ SEQUENCE 107 AA; 12149 MW; 96CCE146450149FE CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

RESULT 15
Q863P7
ID Q863P7 PRELIMINARY; PRT; 107 AA.
AC Q863P7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Growth hormone receptor (Fragment).
GN GHR.
OS Martes americana (American marten).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC Martes.
OX NCBI_TaxID=9660;
RN [1];
RP SEQUENCE FROM N.A.
RA Koepfli K.-P., Wayne R.K.;
RT "Type-1 STS Markers Are More Informative Than Cytochrome b in
RT Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora).";
RL Syst. Biol. 0:0-0(2003).
DR EMBL; AF498196; AAP19687.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON TER 1
FT NON TER 107 107
SQ SEQUENCE 107 AA; 12172 MW; 96BDB14658B649FE CRC64;

Query Match 100.0%; Score 55; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSWVEFIELD 10
Db 31 DSWVEFIELD 40

Search completed: June 9, 2004, 15:51:22
Job time : 33.5135 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2004, 15:36:10 ; Search time 35 seconds  
(without alignments)  
56.510 Million cell updates/sec

Title: US-09-660-302D-7

Perfect score: 43

Sequence: 1 CEEDFYR 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_29Jan04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query	Match Length	DB ID	Description
1	43	100.0	7	2	AAY32791	Aay32791 Proteolyt
2	38	88.4	9	5	ABG94867	Abg94867 Human hGH
3	38	88.4	9	7	AD82293	Ad82293 Plasmid p
4	38	88.4	33	2	AAR22456	Aar22456 Plasmid p
5	38	88.4	246	2	AAR56389	Aar56389 Human gro
6	38	88.4	249	2	AAR06867	Aar06867 Hormone b
7	38	88.4	269	2	AAR05045	Aar05045 Soluble h
8	38	88.4	269	2	AAM10426	Aaw10426 Human som
9	38	88.4	269	2	AAY31767	Aay31767 Human sol
10	38	88.4	269	2	AAR2802	Aaw2802 Human sol
11	38	88.4	269	3	AAY78429	Aay78429 Soluble p
12	38	88.4	269	7	AD82252	Ad82252 Plasmid p
13	38	88.4	315	5	Aau75499	Aau75499 Human fus
14	38	88.4	340	5	Aau75496	Aau75496 Human fus
15	38	88.4	637	1	AAP92108	Aap92108 Human gro
16	38	88.4	638	1	AAP81326	Aap81326 Human gro
17	38	88.4	638	2	AAR33394	Aar33394 Human gro
18	38	88.4	638	7	AD445067	Ad445067 Human gro
19	38	88.4	638	7	AD445063	Ad445063 Human gro
20	38	88.4	648	4	AB811437	Ab811437 Human gro
21	37	86.0	460	6	ABU33279	Abu33279 Protein e
22	36	83.7	84	2	AAY30432	Aay30432 Mature ne
23	36	83.7	84	3	AB815317	Aab15317 A. caninu
24	36	83.7	91	2	AAR91701	Aar91701 AcanAPC2.
25	36	83.7	91	2	AAY30393	Aay30393 Nematode

## ALIGNMENTS

## RESULT 1

AAY32791

ID AAY32791 standard; peptide; 7 AA.

XX AC AAY32791;

XX 09-NOV-1999 (first entry)

DE Proteolytic cleavage signal site used in inhibiting receptor proteolysis.

XX Signal transduction; proteolytic cleavage; cleavage signal site;

KW ubiquitin; proteosome binding site; muscle wasting; renal tubular defect;

KW uraemia; diabetes; Cushing's disease; eating disorder; AIDS;

KW growth hormone deficiency.

XX Mammalia.

OS EP943624-A1.

PN EP943624-A1.

XX 22-SEP-1999.

PD 12-MAR-1998; 98EP-00200799.

XX 12-MAR-1998; 98EP-00200799.

XX (UYUT-) RIJKSUNIV UTRECHT.

XX WPI; 1999-510568/43.

XX Controlling the availability and/or signal transduction capability of a

XX cell surface receptor, useful for treating growth hormone deficiencies.

XX Claim 15; Page 27; 36pp; English.

XX This sequence is a cleavage signal site. This site is used in a method

XX for controlling the availability and signal transduction capability of a

XX cell surface receptor by administering an inhibitor that is capable of

XX inhibiting proteolytic cleavage of the receptor. Inhibition of this

XX proteolytic cleavage results in the receptors being present on the

XX surface for longer and therefore signalling for longer to the interior of

XX the cell. This increases the sensitivity of cells to any hormones which

XX might be present. The inhibitor is derived from or competes with an amino

XX acid sequence around this proteolytic cleavage signal. The inhibitor may

XX be used to treat muscle wasting, associated with disorders such as renal

XX tubular defects, uraemia, diabetes, Cushing's syndrome, cachexias, eating

XX disorders, AIDS, after stress and during neuromuscular disease

XX Sequence 7 AA;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Query Match 100.0%; Score 43; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7  
 |||||  
 Db 1 CEEDFYR 7

RESULT 2  
 ABG94867  
 ID ABG94867 standard; peptide; 9 AA.

XX AC ABG94867;  
 XX 03-DEC-2002 (first entry)  
 XX Human hGH binding protein carboxy terminus from pbGhr(1-246).

XX DE Growth hormone; placental lactogen; prolactin; active domain; hGH; human;  
 KW structure-function relationship; p01446; somatogenic receptor;  
 KW segment-substituted polypeptide; hGH binding protein; mutant; mutein.

XX OS Homo sapiens.  
 XX Synthetic.

XX PN US6428954-B1.

XX 06-AUG-2002.

XX 06-JUN-1995; 95US-00483039.

XX 28-OCT-1988; 88US-00264611.

XX 26-OCT-1989; 89US-00428066.

XX 27-APR-1992; 92US-00875204.

XX 13-OCT-1992; 92US-00960227.

XX 02-FEB-1994; 94US-00190723.

XX (GETH ) GENENTECH INC.

XX Wells JA, Cunningham BC;

XX WPI; 2002-696875/75.

XX N-PSDB; AB873022.

XX Identifying active domains within cloned polypeptides of known amino acid

XX sequence by substituting analog segments into the parent polypeptide is

XX useful to determine the relationship between structure and function.

XX Example 3; Col 31-32; 86pp; English.

XX The invention relates to identifying an unknown active domain in a region  
 CC of known amino acid sequence in a parent polypeptide e.g. human growth  
 CC hormone (hGH) which has been cloned and has a pre-identified biological  
 CC activity, where the active domain interacts with a target when the parent  
 CC polypeptide is in its native-folded form and the interaction is  
 CC responsible for the biological activity comprising: (a) comparing the  
 CC amino acid sequence or polypeptide structure in the region of known amino  
 CC acid sequence of hGH with the amino acid sequence of polypeptide  
 CC structure in a region of known amino acid sequence of an analogue  
 CC polypeptide (e.g. prolactin, placental lactogen or porcine growth  
 CC hormone) which has at least 15% homology with hGH alpha-carbon  
 CC coordinates within about 2-3.5 angstroms of hGH alpha-carbon coordinates  
 CC for about 60% of the analogue sequence, where any interaction of the  
 CC analogue with the target is different from target interaction with hGH;

CC (b) substituting DNA encoding an analogous polypeptide segment from the  
 CC analogue into DNA encoding the full length hGH, and expressing a segment-  
 CC substituted polypeptide; (c) contacting the segment-substituted  
 CC polypeptide with the target to determine interaction; (d) repeating steps  
 CC (b) and (c) with a second analogous polypeptide segment; and (e)  
 CC comparing the difference between activity of the first and second segment  
 CC -substituted polypeptides as an indication of the location of the unknown

CC active domain in hGH. The method is useful for determining the  
 CC relationship between structure and function of known polypeptide  
 CC sequences. The present sequence shows a mutated part of an hGH binding  
 CC protein, a target polypeptide for hGH used to test the binding of  
 CC substitution mutants in the method of the invention

XX Sequence 9 AA;

Query Match 88.4%; Score 38; DB 5; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6  
 |||||  
 Db 4 CEEDFY 9

RESULT 3

ADE82293

ID ADE82293 standard; peptide; 9 AA.

XX AC ADE82293;

XX 29-JAN-2004 (first entry)

XX plasmid phGhr (1-246) carboxy peptide fragment.

XX human growth hormone; hGH; variant; somatogenic receptor.

XX Synthetic.

XX US6451561-B1.

XX 17-SEP-2002.

XX 07-JUN-1995; 95US-00486474.

XX 28-OCT-1988; 88US-00264611.

XX 26-OCT-1989; 89US-00428066.

XX 27-APR-1992; 92US-00875204.

XX 13-OCT-1992; 92US-00960227.

XX 02-FEB-1994; 94US-00190723.

XX (GETH ) GENENTECH INC.

XX Wells JA, Cunningham BC;

XX WPI; 2003-101735/09.

XX N-PSDB; ADE82294.

XX Forming human growth hormone (hGH) variants by substitution mutation so

XX that the variant binds to a target for hGH, e.g. hGH receptors or human

XX prolactin receptors with affinity different from that of wild-type hGH.

XX Example 3; Col 31-32; 87pp; English.

XX This invention describes a method for generating a novel human growth  
 CC hormone (hGH) variant that binds to a target for hGH with an affinity  
 CC different from affinity of wild type hGH for the target. Human growth  
 CC hormone (hGH) has a positive binding activity with the target receptor,  
 CC the somatogenic receptor. The human prolactin (hPRL), human placental  
 CC lactogen (hPL) and porcine growth hormone (pGH) analogues, however, have  
 CC a greatly reduced activity with that target. Six segment-substituted  
 CC growth hormones were formed by substituting selected amino acid segments  
 CC of hGH with an analogous amino acid segment from the analogue. Each of  
 CC these selected segments are different and were chosen to probe either the  
 CC entire amino acid sequence of the hGH molecule or those regions which are  
 CC expected to contain the active domains. This sequence represents a  
 CC fragment of plasmid phGhr used in the generation of hGH binding protein  
 CC constructions.

XX Sequence 9 AA;

Query Match 88.4%; Score 38; DB 7; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6  
 DB 4 CEEDFY 9

RESULT 4  
 AAR22456  
 ID AAR22456 standard; protein; 33 AA.

XX AC AAR22456;  
 XX DT 09-SEP-1992 (first entry)  
 XX DE Plasmid pBSR8-3 encoded polypeptide.  
 XX KW Recombinant; plasmid pAcYmHGHR; hGHR binding region;  
 XX KW human growth hormone.  
 XX OS Synthetic.  
 XX PN JF04063594-A.  
 XX PD 28-FEB-1992.  
 XX PF 03-JUL-1990; 90JP-00176630.  
 XX PR 03-JUL-1990; 90JP-00176630.  
 XX PA (TANP-) TANPAKU KAGAKU KENK.  
 XX DR WPI; 1992-120154/15.  
 XX DR N-PSDB; AAQ23311.

XX PT New recombinant plasmid and Baculovirus having specific DNA fragment -  
 XX PT used for prep. of hormone binding region protein of human growth hormone  
 XX PT receptor.  
 XX PS Example; Fig 2; 11pp; Japanese.

XX CC The sequence is that encoded by a fragment of the plasmid pBSR8-3 which  
 XX CC is used in the construction of plasmid pAcYmHGHR. pAcYmHGHR contains a  
 XX CC DNA fragment encoding the binding region of human growth hormone receptor  
 XX CC (hGHR) under control of a Baculovirus gene expression system. This can be  
 XX CC used to transform insect cells to produce a more natural protein than is  
 XX CC obtd. with E.coli and in larger amts. See also AAR22457-R22459  
 XX SQ Sequence 33 AA;

Query Match 88.4%; Score 38; DB 2; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 3.3;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6  
 DB 28 CEEDFY 33

RESULT 5  
 AAR56389  
 ID AAR56389 standard; protein; 246 AA.

XX AC AAR56389;  
 XX DT 01-MAR-1995 (first entry)  
 XX DE Human growth hormone receptor C-domain.  
 XX KW Human growth hormone receptor; hGHR; C-domain; CD; hGHR-CD;  
 XX KW extracellular; enhancement; Met130Q-238Q; GS129V-238Q.

XX OS Homo sapiens.  
 XX PN JF06172394-A.  
 XX PD 21-JUN-1994.  
 XX PF 10-DEC-1992; 92JP-00330361.  
 XX PR 10-DEC-1992; 92JP-00330361.  
 XX PA (TANP-) TANPAKU KOGAKU KENKYUSHO KK.  
 XX DR WPI; 1994-238767/29.

XX PT Extracellular C-domain protein of growth hormone receptor (hGHR-CD) - is  
 XX PT used to enhance growth hormone function.  
 XX PS Disclosure; Page 9-10; 16pp; Japanese.

XX CC The extracellular C-domain of hGHR is used to enhance growth hormone  
 XX CC function. Two forms, Met130Q-238Q (AAQ66550) and GS129V-238Q (AAQ66553)  
 XX CC are given. Primers for the isolation of extracellular hGHR-CD are given  
 XX CC in AAQ66551-52 and AAQ66554-55

XX SQ Sequence 246 AA;

Query Match 88.4%; Score 38; DB 2; Length 246;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6  
 DB 241 CEEDFY 246

RESULT 6  
 AAR06867  
 ID AAR06867 standard; protein; 249 AA.

XX AC AAR06867;  
 XX DT 16-JAN-1991 (first entry)  
 XX DE Hormone binding region of human growth hormone receptor.  
 XX KW hGHR.  
 XX OS Synthetic.  
 XX PN JF02200186-A.  
 XX PD 08-AUG-1990.  
 XX PF 30-JAN-1989; 89JP-00020182.  
 XX PR 30-JAN-1989; 89JP-00020182.

XX PA (TANP-) TANPAKU KOGAKU KENK.  
 XX DR WPI; 1990-285858/38.  
 XX DR N-PSDB; AAQ05968.

XX PT Synthetic gene - used for coding the amino acid sequence in the hormone-  
 XX PT combining region of human growth hormone receptor.

XX PS Disclosure; Fig 2; 11pp; Japanese.

XX CC The sequence is the same as that of the natural receptor but is encoded  
 XX CC by a synthetic gene that has a slightly altered nucleotide sequence  
 XX CC incorporating at least 2 new restriction sites and removing a direct  
 XX CC repeat and a palindromic sequence

SQ Sequence 249 AA;  
 Query Match 88.4%; Score 38; DB 2; Length 249;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CEEDFY 6  
 Db 241 CEEDFY 246  
 |||||  
 RESULT 7  
 AAR05045  
 ID AAR05045 standard; protein; 269 AA.  
 XX AAR05045;  
 AC  
 XX 25-MAR-2003 (revised)  
 DT 03-OCT-1990 (first entry)  
 XX  
 XX Soluble human growth hormone receptor.  
 DE  
 XX Plasmid pJ1446; human growth hormone; somatogenic receptor; mutagenesis;  
 KW substitutions; active domain; hormone variants.  
 XX  
 XX Synthetic.  
 OS  
 XX WO9004788-A.  
 PN  
 XX 03-MAY-1990.  
 PD  
 XX 28-OCT-1988; 88US-00264611.  
 PF  
 XX 28-OCT-1988; 88US-00264611.  
 PR  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Wells JA, Cunningham BC;  
 PI  
 WPI; 1990-164120/21.  
 DR N-PSDB; AAQ04672.  
 XX  
 XX Identifying active domains and aminoacid(s) in polypeptide(s) - by  
 PT specific substitutions, then testing modified products for interaction  
 PT with target, and new polypeptide, esp. hormone etc.  
 PT  
 XX Disclosure; Page ?; 193pp; English.  
 XX  
 CC The soluble human growth hormone receptor shGhr was subcloned into pBO475  
 CC to form pJ1446. E.coli W3110, degp was transformed with pJ1446 and grown  
 CC in low-phosphate media in a fermentor at 30 degrees C. This 246 amino  
 CC acid hGhr is produced. See also AAQ04671 and AAQ04672. (Updated on 25-MAR  
 CC -2003 to correct PR field.)  
 XX  
 SQ Sequence 269 AA;  
 Query Match 88.4%; Score 38; DB 2; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CEEDFY 6  
 Db 264 CEEDFY 269  
 |||||  
 RESULT 8  
 AAW10426  
 ID AAW10426 standard; protein; 269 AA.  
 XX AAW10426;  
 AC  
 XX 25-MAR-2003 (revised)  
 DT 11-AUG-1997 (first entry)

XX Human somatogenic receptor extracellular domain.  
 DE  
 XX Active site; active domain; growth hormone; somatogenic receptor;  
 KW mutagenesis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH Peptide 1..23  
 FT /label= Sig\_peptide  
 FT 24..269  
 FT Protein /label= Mat\_protein  
 FT /note= "shGhr(aal-246)"  
 XX  
 XX US5580723-A.  
 PN  
 XX 03-DEC-1996.  
 PD  
 XX 02-FEB-1994; 94US-00190723.  
 PF  
 XX 28-OCT-1988; 88US-00264611.  
 PR 26-OCT-1989; 89US-00428066.  
 PR 27-APR-1992; 92US-00875204.  
 PR 13-OCT-1992; 92US-00960227.  
 PR  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Cunningham BC, Wells JA;  
 PI  
 WPI; 1997-033563/03.  
 DR N-PSDB; AAT10426.  
 XX  
 XX Identification of unknown active domains in polypeptide(s) - useful for  
 PT analysis of structure and function of hormones, etc.  
 PT  
 XX Example 3; Fig 12A-C; 86pp; English.  
 XX  
 CC A polypeptide (AAW10426) comprises the soluble extracellular domain of  
 CC human liver growth hormone receptor (somatogenic receptor, shGhr). It was  
 CC expressed in Escherichia coli transformants using a vector derived from  
 CC pJ1446 (AAT47449). shGhr can be used in a novel method designed for the  
 CC identification of polypeptide active domains. For human growth hormone  
 CC (hGH) (see also AAW10425), this involves substituting selected amino acid  
 CC segments of hGH with analogous segments from analogue polypeptides (human  
 CC placenta lactogen, human prolactin and pig growth hormone) and examining  
 CC the effect of the substn. on binding affinity to shGhr. Once active site  
 CC regions are detd., active site amino residues (see also AAW10427-62) can  
 CC be similarly identified. (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 269 AA;  
 Query Match 88.4%; Score 38; DB 2; Length 269;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CEEDFY 6  
 Db 264 CEEDFY 269  
 |||||  
 RESULT 9  
 AAY31767  
 ID AAY31767 standard; protein; 269 AA.  
 XX AAY31767;  
 AC  
 XX 06-DEC-1999 (first entry)  
 DT  
 XX Human soluble growth hormone receptor.  
 DE  
 XX Growth hormone receptor; somatogenic receptor; human; pJ1446; variant;  
 KW protein engineering.



```

XX OS Homo sapiens.
XX FH Key
XX FT Peptide Location/Qualifiers
XX FT /label= "signal peptide"
XX FT /note= "mature protein"
XX FT
XX FT
XX PN US5955346-A.
XX XX
XX PD 21-SEP-1999.
XX XX
XX XX 07-JUN-1995; 95US-00476999.
XX PR 28-OCT-1988; 88US-00264611.
XX PR 26-OCT-1989; 89US-00428066.
XX PR 27-APR-1992; 92US-00875204.
XX PR 13-OCT-1992; 92US-00960227.
XX PR 02-FEB-1994; 94US-00190723.
XX PR 02-FEB-1994; 94US-00190723.
XX PA (GETH ) GENENTECH INC.
XX PI Cunningham BC, Wells JA;
XX PI WPI; 1999-560495/47.
XX DR N-PSDB; AAX87977.
XX XX
XX PT Isolated nucleic acids encoding variants of human prolactin and placental
XX PT lactogen useful for identifying active domains within those proteins.
XX PS Example 2; Fig 12A-C; 86pp; English.
XX XX
XX CC This sequence represents a human soluble growth hormone receptor (shGHR)
XX CC encoded by plasmid pJ1446 (see AAX87977). shGHR was expressed in E. coli
XX CC and was used in binding assays of human growth hormone variants. The
XX CC invention provides a method for the systematic analysis of the structure
XX CC and function of polypeptides by identifying active domains which
XX CC influence the activity of the polypeptide with a target substance, and a
XX CC method for identifying the active amino acid residues within the active
XX CC domain of a polypeptide. It also provides polypeptide variants comprising
XX CC segment-substituted and residue-substituted growth hormones, prolactins
XX CC (see AAX31764) and placental lactogens (see AAX31765). Identifying
XX CC receptor binding sites in hormones permits the rational design of
XX CC receptor specific variants
XX CC
XX SQ Sequence 269 AA;
XX
XX Query Match 88.4%; Score 38; DB 2; Length 269;
XX Best Local Similarity 100.0%; Pred. No. 27;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CEDDFY 6
Db 264 CEDDFY 269

RESULT 10
AAW82802
XX ID AAW82802 standard; protein; 269 AA.
XX AC AAW82802;
XX XX
XX DT 01-MAR-1999 (first entry)
XX DE Human soluble somatogenic receptor.
XX XX
XX KW Somatogenic receptor; growth hormone; human; plasmid pJ1446;
XX KW active domain.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers

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FT Peptide 1..23
FT Protein /label= Sig_peptide
FT 24..269
FT /label= Mat_protein
XX US5834250-A.
XX PD 10-NOV-1998.
XX XX
XX PF 30-JUN-1997; 97US-00903398.
XX XX
XX PR 28-OCT-1988; 88US-00264611.
XX PR 26-OCT-1989; 89US-00428066.
XX PR 27-APR-1992; 92US-00875204.
XX PR 13-OCT-1992; 92US-00960227.
XX PR 02-FEB-1994; 94US-00190723.
XX PR 06-JUN-1995; 95US-00483039.
XX PA (GETH ) GENENTECH INC.
XX PI Cunningham BC, Wells JA;
XX PI WPI; 1999-008714/01.
XX DR N-PSDB; AAV62766.
XX XX
XX PT Identifying amino acids in polypeptide(s) that are involved in
XX PT interaction with target - by introducing scanning amino acid
XX PT substitutions at selected positions and screening for any change in
XX PT interaction, particularly to engineer hormones with altered properties.
XX PS Example 3; Fig 12A-J; 84pp; English.
XX XX
XX CC This is the amino acid sequence of human liver soluble somatogenic
XX CC receptor, as encoded by a DNA insert of plasmid pJ1446 (see AAV62766).
XX CC The invention provides methods for the systematic analysis of the
XX CC structure and function of polypeptides by identifying active domains
XX CC which influence the activity of the polypeptide with a target substance
XX CC (for human growth hormone (see AAW82801, the target used was somatogenic
XX CC receptor). Active domains are determined by substituting selected amino
XX CC acid segments of the polypeptide with an analogous polypeptide segment,
XX CC and comparing the activity of the substituted polypeptide with that of
XX CC the native polypeptide for the target. The invention also provides
XX CC methods for identifying the active amino acids within the active domain.
XX CC The method is particularly applied to hormones. Polypeptides can be
XX CC produced that have better biological, biochemical and immunogenic
XX CC properties than wild-type proteins, e.g. human growth hormone with
XX CC increased potency but reduced diabetogenic activity and human prolactin
XX CC or placental lactogen may have increased activity at somatogenic
XX CC receptors
XX XX
XX SQ Sequence 269 AA;
XX
XX Query Match 88.4%; Score 38; DB 2; Length 269;
XX Best Local Similarity 100.0%; Pred. No. 27;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CEDDFY 6
Db 264 CEDDFY 269

RESULT 11
AAW78429
XX ID AAY78429 standard; protein; 269 AA.
XX AC AAY78429;
XX XX
XX DT 09-MAY-2000 (first entry)
XX DE Soluble part of the somatogenic receptor encoded by plasmid pJ1446.
XX KW Human growth hormone; hGH; prolactin; placental lactogen; modification;
XX KW mutagenesis.

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XX OS Homo sapiens.
XX OS Synthetic.
XX PN US6013478-A.
XX PD 11-JAN-2000.
XX PF 24-JUN-1998; 98US-00104036.
XX PR 28-OCT-1988; 88US-00264611.
XX PR 26-OCT-1989; 89US-00428066.
XX PR 27-APR-1992; 92US-00875204.
XX PR 13-OCT-1992; 92US-00960227.
XX PR 02-FEB-1994; 94US-00190723.
XX PR 06-JUN-1995; 95US-00483039.
XX PR 30-JUN-1997; 97US-00903398.
XX PA (GETH ) GENENTECH INC.
XX PI Wells JA, Cunningham BC;
XX PN WPI; 2000-159873/14.
XX PR N-PSDB; AAZ88448.
XX PT Recombinant production of variant polypeptides, e.g. growth hormone
XX PT variants with altered receptor specificity, using cells transformed with
XX PT DNA selected by scanning mutagenesis in at least one peptide domain.
XX PS Example 3; Fig 12; 83pp; English.
XX CC The present invention describes the production of a polypeptide variant
XX CC (I) comprising segment substituted and residue substituted growth
XX CC hormone, prolactin or placental lactogens. The method is particularly
XX CC used to produce variants of growth hormone (GH), prolactin or placental
XX CC lactogen, but may also be applied to receptors, interferons, and colony-
XX CC stimulating factors. A particular application is the production of human
XX CC GH variants with altered (decreased or increased) binding interaction
XX CC with the somatogenic receptor, i.e. compounds useful as human GH
XX CC (antagonists and which may have higher potency for stimulating other
XX CC human GH receptors, and as standards or tracers in immunoassays for human
XX CC GH. This method of DNA selection identifies the biologically active
XX CC residues in active domains, including those critical for interaction with
XX CC different targets. The present sequence represents the soluble region of
XX CC the somatogenic receptor from liver encoded by a plasmid, which is used
XX CC in the exemplification of the present invention
XX SQ Sequence 269 AA;
Query Match 88.4%; Score 38; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CEEDFY 6
Db 264 CEEDFY 269
RESULT 12
ADE82252
XX ID ADE82252 standard; protein; 269 AA.
XX AC ADE82252;
XX XX 29-JAN-2004 (first entry)
XX DE Plasmid pBJ1446 containing growth hormone (hGH) protein.
XX KW human growth hormone; hGH; variant; somatogenic receptor; circular.
XX OS Synthetic.
XX PN US6451561-B1.

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XX PD 17-SEP-2002.
XX PF 07-JUN-1995; 95US-00486474.
XX PR 28-OCT-1988; 88US-00264611.
XX PR 26-OCT-1989; 89US-00428066.
XX PR 27-APR-1992; 92US-00875204.
XX PR 13-OCT-1992; 92US-00960227.
XX PR 02-FEB-1994; 94US-00190723.
XX PA (GETH ) GENENTECH INC.
XX PI Wells JA, Cunningham BC;
XX PN WPI; 2003-101735/09.
XX PR N-PSDB; ADE82251.
XX PT Forming human growth hormone (hGH) variants by substitution mutation so
XX PT that the variant binds to a target for hGH, e.g. hGH receptors or human
XX PT prolactin receptors with affinity different from that of wild-type hGH.
XX PS Example 3; Fig 12A-C; 87pp; English.
XX CC This invention describes a method for generating a novel human growth
XX CC hormone (hGH) variant that binds to a target for hGH with an affinity
XX CC different from affinity of wild type hGH for the target. Human growth
XX CC hormone (hGH) has a positive binding activity with the target receptor,
XX CC the somatogenic receptor. The human prolactin (hPRL), human placental
XX CC lactogen (hPL) and porcine growth hormone (pGH) analogues, however, have
XX CC a greatly reduced activity with that target. Six segment-substituted
XX CC growth hormones were formed by substituting selected amino acid segments
XX CC of hGH with an analogous amino acid segment from the analogue. Each of
XX CC these selected segments are different and were chosen to probe either the
XX CC entire amino acid sequence of the hGH molecule or those regions which are
XX CC expected to contain the active domains. This sequence represents the
XX CC plasmid pJ1466 which contains the synthetic hGH described in the
XX CC disclosure of the invention.
XX SQ Sequence 269 AA;
Query Match 88.4%; Score 38; DB 7; Length 269;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CEEDFY 6
Db 264 CEEDFY 269
RESULT 13
AAU75499
XX ID AAU75499 standard; protein; 315 AA.
XX AC AAU75499;
XX XX 08-MAY-2002 (first entry)
XX DE Human fusion protein Chi 1A2.
XX KW Human; GHS1-23; human growth hormone; GH; GHR; growth hormone; receptor;
XX KW GHtopGHR SD100; GHlinkGHR; GHlinkGHRflec; pTcrnssac1; TrcHindrev;
XX KW Chi 1A2 chimera; acromegaly; gigantism; growth hormone deficiency;
XX KW Turner's syndrome; renal failure; osteoporosis; diabetes mellitus;
XX KW cancer; obesity; insulin resistance; hyperlipidaemia; hypertension;
XX KW anaemia; autoimmune disease; infectious disease; inflammatory disorder;
XX KW rheumatoid arthritis; interleukin-6 chimera; IL-6.
XX OS Homo sapiens.
XX XX Key Location/Qualifiers
XX FT Misc-difference 14
XX FT /note= "Encoded by ATG"

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FT Misc-difference 312 /label= Unknown
FT /note= "Encoded by TGA, in-frame stop codon"
FT Misc-difference 313 /label= Unknown
FT /note= "Encoded by TAA, in-frame stop codon"
PN WO200196565-A2.
XX 20-DEC-2001.
XX 18-JUN-2001; 2001WO-GB002645.
XX 16-JUN-2000; 2000GB-00014765.
PR 10-MAR-2001; 2001GB-00005969.
PR 16-MAR-2001; 2001GB-00006487.
XX (ASTE-) ASTERION LTD.
XX Ross R, Artymiuik P, Sayers J;
XX WPI; 2002-130734/17.
DR N-PSDB; ABK14547.
XX
XX New binding agent useful in producing a medicament for treating e.g.
PT cancer, obesity, acromegaly or gigantism, comprises a first part that
PT binds to a ligand binding domain of a receptor and a second part having a
PT receptor binding domain.
XX
XX Claim 49; Fig 22; 79pp; English.
XX
XX The invention relates to a binding agent comprising a first part capable
CC of binding a ligand binding domain of a receptor linked to a second part
CC comprising a receptor binding domain, where the binding agent modulates
CC the activity of the receptor. Also included are a nucleic acid molecule
CC having a sequence, which encodes a binding agent comprising sequences
CC given in the specification comprising the sequences of the full length
CC GHstopGHR SD100 construct, GHlinkGHR construct (GH, growth hormone, GHR,
CC growth hormone receptor), GHlinkGHRflec construct, 1157 base pair PCR
CC fragment GHlinkGHR generated by nucleotides pTRCNSsacI and TrcHindrev,
CC or the nucleotide sequence of the Chi 1A2 chimera, sequences binding to
CC the nucleic acids or degenerate sequences representing them (which have
CC receptor antagonising activity), their encoded polypeptides, a vector
CC comprising the nucleic acids and a cell transformed/transfected with the
CC nucleic acid or vector. The binding agent is useful for manufacturing a
CC medicament for the treatment of acromegaly, gigantism, growth hormone
CC (GH) deficiency, Turner's syndrome, renal failure, osteoporosis, diabetes
CC mellitus, cancer, obesity, insulin resistance, hyperlipidaemia,
CC hypertension, anaemia, autoimmune and infectious diseases, and
CC inflammatory disorders including rheumatoid arthritis (interleukin (IL)-6
CC chimera). The present sequence represents the fusion protein agent of
CC the invention being the Chi 1A2 construct (growth hormone/growth hormone
CC receptor not linked by a synthetic peptide linker)
XX
SQ Sequence 315 AA;
Query Match 88.4%; Score 38; DB 5; Length 315;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CEDDFY 6
Db 306 CEDDFY 311
|||||
RESULT 14
AAU75496
ID AAU75496 standard; protein; 340 AA.
XX AAU75496;
XX
XX 08-MAY-2002 (first entry)
XX

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DE Human fusion protein GHlinkGHR.
XX
KW Human; GHS1-23; human growth hormone; GH; GHR; growth hormone; receptor;
KW GHstopGHR SD100; GHlinkGHR; GHlinkGHRflec; pTRCNSsacI; TrcHindrev;
KW Chi 1A2 chimera; acromegaly; gigantism; growth hormone deficiency;
KW Turner's syndrome; renal failure; osteoporosis; diabetes mellitus;
KW cancer; obesity; insulin resistance; hyperlipidaemia; hypertension;
KW anaemia; autoimmune disease; infectious disease; inflammatory disorder;
KW rheumatoid arthritis; interleukin-6 chimera; IL-6.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 14 /note= "Encoded by ATG"
FT Misc-difference 337 /label= Unknown
FT /note= "Encoded by TGA, in-frame stop codon"
FT Misc-difference 338 /label= Unknown
FT /note= "Encoded by TAA, in-frame stop codon"
XX WO200196565-A2.
XX
XX 20-DEC-2001.
XX
XX 18-JUN-2001; 2001WO-GB002645.
XX
XX 16-JUN-2000; 2000GB-00014765.
PR 10-MAR-2001; 2001GB-00005969.
PR 16-MAR-2001; 2001GB-00006487.
XX
XX (ASTE-) ASTERION LTD.
XX
XX Ross R, Artymiuik P, Sayers J;
XX WPI; 2002-130734/17.
DR N-PSDB; ABK14531.
XX
XX New binding agent useful in producing a medicament for treating e.g.
PT cancer, obesity, acromegaly or gigantism, comprises a first part that
PT binds to a ligand binding domain of a receptor and a second part having a
PT receptor binding domain.
XX
XX Disclosure; Fig 6; 79pp; English.
XX
XX The invention relates to a binding agent comprising a first part capable
CC of binding a ligand binding domain of a receptor linked to a second part
CC comprising a receptor binding domain, where the binding agent modulates
CC the activity of the receptor. Also included are a nucleic acid molecule
CC having a sequence, which encodes a binding agent comprising sequences
CC given in the specification comprising the sequences of the full length
CC GHstopGHR SD100 construct, GHlinkGHR construct (GH, growth hormone, GHR,
CC growth hormone receptor), GHlinkGHRflec construct, 1157 base pair PCR
CC fragment GHlinkGHR generated by nucleotides pTRCNSsacI and TrcHindrev,
CC or the nucleotide sequence of the Chi 1A2 chimera, sequences binding to
CC the nucleic acids or degenerate sequences representing them (which have
CC receptor antagonising activity), their encoded polypeptides, a vector
CC comprising the nucleic acids and a cell transformed/transfected with the
CC nucleic acid or vector. The binding agent is useful for manufacturing a
CC medicament for the treatment of acromegaly, gigantism, growth hormone
CC (GH) deficiency, Turner's syndrome, renal failure, osteoporosis, diabetes
CC mellitus, cancer, obesity, insulin resistance, hyperlipidaemia,
CC hypertension, anaemia, autoimmune and infectious diseases, and
CC inflammatory disorders including rheumatoid arthritis (interleukin (IL)-6
CC chimera). The present sequence represents the fusion protein agent of
CC the invention being the GHlinkGHR construct (growth hormone/growth
CC hormone receptor linked by a synthetic peptide linker)
XX
SQ Sequence 340 AA;
Query Match 88.4%; Score 38; DB 5; Length 340;

```

Best Local Similarity 100.0%; Pred. No. 35;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6  
Db 331 CEEDFY 336  
|||||

RESULT 15  
AAP92108  
ID AAP92108 standard; protein; 637 AA.

XX AC AAP92108;  
XX DT 14-FEB-1990 (first entry)  
XX DE Human growth hormone receptor.  
XX KW Growth hormone receptor.  
XX OS Homo sapiens.  
XX FN US4857637-A.  
XX PD 15-AUG-1989.  
XX PF 12-JUN-1987; 87US-00061942.  
XX PR 22-MAY-1985; 85US-00737302.  
XX PR 07-MAY-1986; 86US-00861236.  
XX PA (GETH ) GENENTECH INC.  
XX PI Hammonds RG, Leung DW, Martin DW, Spencer SA, Wood WI;  
XX DR WPI; 1989-300419/41.  
XX DR N-PSDE; AAN91325.  
XX PT Modulating growth hormone receptor activity - by immunising animal  
PT against growth hormone receptor extracellular domain deriv. to raise  
PT antiserum.  
XX PS Disclosure; Fig 2a-c; 18pp; English.  
XX CC An animal can be immunised against its growth hormone receptor by  
CC vaccinating against a growth hormone receptor extracellular domain deriv.  
CC predetermined to raise polyclonal antiserum which affect the receptor as a  
CC growth hormone agonist. This method enables continuous growth of target  
CC tissues without frequent hormone admin  
XX SQ Sequence 637 AA;

Query Match 88.4%; Score 38; DB 1; Length 637;  
Best Local Similarity 100.0%; Pred. No. 66;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6  
Db 259 CEEDFY 264  
|||||

Search completed: June 9, 2004, 15:48:28  
Job time : 36 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 9, 2004, 15:43:40 ; Search time 7.75676 Seconds  
(without alignments)  
86.807 Million cell updates/sec

Title: US-09-660-302D-7

Perfect score: 43

Sequence: 1 CEDDFYR 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:\*  
1: piri:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	88.4	638	2	somatotropin recep
2	36	83.7	364	1	transforming prote
3	36	83.7	368	1	transforming prote
4	36	83.7	378	1	LJM domain-contain
5	36	83.7	400	2	LJM domain-contain
6	36	83.7	426	1	homeotic protein L
7	36	83.7	726	2	homeotic protein L
8	35	81.4	202	2	hypothetical prote
9	35	81.4	552	2	conserved hypotet
10	35	81.4	1376	2	collagen alpha 5 c
11	35	81.4	1822	2	collagen alpha 2 c
12	35	81.4	3198	2	collagen alpha 2 f
13	34	79.1	277	2	hypothetical prote
14	34	79.1	331	2	L-asparaginase (im
15	34	79.1	563	2	DNA repair helicase
16	34	79.1	599	2	sterol esterase (E
17	34	79.1	612	2	sterol esterase (E
18	34	79.1	625	2	hypothetical integ
19	34	79.1	707	1	ribonucleoside-tri
20	33	76.7	86	2	hypothetical prote
21	33	76.7	272	2	conserved hypotet
22	33	76.7	441	2	CRF MSV250 hypotet
23	33	76.7	496	2	hypothetical prote
24	32	74.4	154	2	aspartate carbamoy
25	32	74.4	200	2	hypothetical prote
26	32	74.4	309	2	Zinc finger, C3HC4
27	32	74.4	352	2	hypothetical prote
28	32	74.4	352	2	hypothetical prote
29	32	74.4	395	1	homeotic protein 1

30	32	74.4	407	2	C86202	hypothetical prote
31	32	74.4	415	2	G83863	threonine dehydrat
32	32	74.4	486	2	JC1415	histamine H1 recep
33	32	74.4	487	2	JC2495	histamine H1 recep
34	32	74.4	488	2	I56507	histamine H1 recep
35	32	74.4	491	2	A41632	histamine H1 recep
36	32	74.4	531	2	G84710	hypothetical prote
37	32	74.4	581	2	B54665	netrin-2 precursor
38	32	74.4	606	2	A54665	netrin-1 precursor
39	32	74.4	647	2	S26386	transcription fact
40	32	74.4	676	2	A81349	probable ATP-depen
41	32	74.4	740	2	F71369	conserved hypotet
42	32	74.4	796	2	T39962	coatamer complex b
43	32	74.4	893	2	S51603	receptor-like tyro
44	32	74.4	898	2	S47489	receptor tyrosine
45	32	74.4	976	2	A36355	protein-tyrosine k

## ALIGNMENTS

### RESULT 1

A33991

somatotropin receptor precursor - human

N;Alternate names: growth hormone receptor

N;Contains: somatotropin-binding protein, serum

C;Species: Homo sapiens (man)

C;Date: 23-Mar-1990 #sequence\_revision 23-Mar-1990 #text\_change 02-Aug-2002

C;Accession: A33991; S04530

R;Godowski, P.J.; Leung, D.W.; Meacham, L.R.; Galgani, J.P.; Hellmiss, R.; Keret, R.; R;

Proc. Natl. Acad. Sci. U.S.A. 86, 8083-8087, 1989

A;Title: Characterization of the human growth hormone receptor gene and demonstration o

A;Reference number: A33991; MUID:90046742; PMID:2813379

A;Accession: A33991

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-638 <GOD>

A;Cross-references: GB:M28458; GB:M28459; GB:M28460; GB:M28461; GB:M28462; GB:M28463; G

R;Leung, D.W.; Spencer, S.A.; Cachianes, G.; Hammonds, R.G.; Collins, C.; Henzel, W.J.;

Nature 330, 537-543, 1987

A;Title: Growth hormone receptor and serum binding protein: purification, cloning and e

A;Reference number: S04530; MUID:88065896; PMID:2825030

A;Accession: S04530

A;Molecule type: mRNA

A;Residues: 1-543, 'I', 545-638 <LEU>

A;Cross-references: EMBL:X06562; NID:g31737; PIDN:CAA29808.1; PID:g31738

C;Genetics:

A;Gene: GDB:GHR

A;Cross-references: GDB:119984; OMIM:600946

A;Map position: 5p13-5p12

C;Superfamily: interleukin-2 receptor beta chain; fibronectin type III repeat homology

C;Keywords: liver; transmembrane protein

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-638/Product: somatotropin receptor #status predicted <MAT>

F;265-288/Domain: transmembrane #status predicted <TM>

Query Match

Best Local Similarity 88.4%; Score 38; DB 2; Length 638;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 CEDDFY 6

Db

259 CEDDFY 264

### RESULT 2

TVHML

transforming protein L-myc-1 - human

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 18-Jun-1999

C;Accession: A27675; S01200; S09390

R;Kaye, F.; Battey, J.; Nau, M.; Brooks, B.; Seifter, E.; De Greve, J.; Birrer, M.; Saus

Mol. Cell. Biol. 8, 186-195, 1988

A;Title: Structure and expression of the human L-myc gene reveal a complex pattern of al  
A;Reference number: A27675; MUID:88094386; PMID:2827002  
A;Accession: A27675  
A;Molecule type: DNA  
A;Residues: 1-364 <KAY>  
A;Cross-references: GB:M19720; NID:g188906; PIDN:AAA59879.1; PID:g386964  
R;DePinho, R.A.; Hatton, K.S.; Tesfaye, A.; Yancopoulos, G.D.; Alt, F.W.  
Genes Dev. 1, 1311-1326, 1987  
A;Title: The human myc gene family: structure and activity of L-myc and an L-myc pseudog  
A;Reference number: S01200; MUID:88112807; PMID:332939  
A;Accession: S01200  
A;Molecule type: DNA  
A;Residues: 1-364 <DBP>  
R;Ikigaki, N.; Minna, J.; Kennett, R.H.  
EMBO J. 8, 1793-1799, 1989  
A;Title: The human L-myc gene is expressed as two forms of protein in small cell lung ca  
A;Reference number: S09390; MUID:8935654; PMID:2548855  
A;Accession: S09390  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 165-179 <IKE>  
C;Genetics:  
A;Gene: GDB:MYCL1  
A;Cross-references: GDB:120706; OMIM:164850  
A;Map position: lp32-lp32  
A;Introns: 166/1  
C;Superfamily: myc transforming protein; myc transforming protein homology  
C;Keywords: DNA binding; nucleus; transforming protein  
F;1-364/Domain: myc transforming protein homology <MYC>  
  
Query Match 83.7%; Score 36; DB 1; Length 364;  
Best Local Similarity 85.7%; Pred. No. 19;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 CEEDFYR 7  
Db 15 CGEDFYR 21  
  
RESULT 3  
TVMSML  
transforming protein L-myc - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1991 #sequence\_revision 31-Mar-1991 #text\_change 18-Jun-1999  
C;Accession: S03017  
R;Legouy, E.; DePinho, R.; Zimmerman, K.; Collum, R.; Yancopoulos, G.; Mitsock, L.; Kri  
EMBO J. 6, 3359-3366, 1987  
A;Title: Structure and expression of the murine L-myc gene.  
A;Reference number: S03017; MUID:88111523; PMID:2828024  
A;Accession: S03017  
A;Molecule type: DNA  
A;Residues: 1-368 <LRG>  
A;Cross-references: GB:X13945; GB:X06183; GB:X13949; GB:Y00082; NID:g53287; PIDN:CAA3212  
C;Genetics:  
A;Gene: L-myc  
C;Superfamily: myc transforming protein; myc transforming protein homology  
C;Keywords: DNA binding; leucine zipper; nucleus; transforming protein  
F;1-368/Domain: myc transforming protein homology <MYC>  
F;337-365/Region: leucine zipper motif  
  
Query Match 83.7%; Score 36; DB 1; Length 368;  
Best Local Similarity 85.7%; Pred. No. 19;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 CEEDFYR 7  
Db 15 CGEDFYR 21  
  
RESULT 4  
JC5658  
LIM domain-containing homeodomain LH-2B - chicken  
C;Species: Gallus gallus (chicken)

C;Date: 17-Nov-1997 #sequence\_revision 17-Nov-1997 #text\_change 15-Oct-1999  
C;Accession: JC5658  
R;Nohno, T.; Kawakami, Y.; Wada, N.; Ishikawa, T.; Ohuchi, H.; Noji, S.  
Biochem. Biophys. Res. Commun. 238, 506-511, 1997  
A;Title: Differential expression of the two closely related LIM-class homeobox genes LH  
A;Reference number: JC5657; MUID:97446014; PMID:9299541  
A;Accession: JC5658  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-378 <NOH>  
A;Cross-references: GB:L35566; NID:g556037; PIDN:AAA50258.1; PID:g556038  
C;Comment: This protein plays a role in the determination and specification of the proxi  
C;Superfamily: homeotic protein LH-2; homeobox homology; LIM metal-binding repeat homol  
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;50-100/Domain: LIM domain 1 #status predicted <LD1>  
F;52-104/Domain: LIM metal-binding repeat homology <LIM>  
F;103-169/Domain: LIM domain 2 #status predicted <LD2>  
F;114-167/Domain: LIM metal-binding repeat homology <LIM1>  
F;246-310/Domain: homeodomain #status predicted <HOM>  
F;249-305/Domain: homeobox homology <HOX>  
  
Query Match 83.7%; Score 36; DB 2; Length 378;  
Best Local Similarity 71.4%; Pred. No. 20;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CEEDFYR 7  
Db 101 CKEDYR 107  
  
RESULT 5  
JC5657  
LIM domain-containing homeodomain LH-2A - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 17-Nov-1997 #sequence\_revision 17-Nov-1997 #text\_change 20-Jun-2000  
C;Accession: JC5657  
R;Nohno, T.; Kawakami, Y.; Wada, N.; Ishikawa, T.; Ohuchi, H.; Noji, S.  
Biochem. Biophys. Res. Commun. 238, 506-511, 1997  
A;Title: Differential expression of the two closely related LIM-class homeobox genes LH  
A;Reference number: JC5657; MUID:97446014; PMID:9299541  
A;Accession: JC5657  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-400 <NOH>  
A;Cross-references: GB:AB005882; NID:g2340818; PIDN:BAA21846.1; PID:g2340819  
C;Comment: This protein plays a role in the determination and specification of the proxi  
C;Superfamily: homeotic protein LH-2; homeobox homology; LIM metal-binding repeat homol  
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;52-102/Domain: LIM domain 1 #status predicted <LD1>  
F;54-106/Domain: LIM metal-binding repeat homology <LIM1>  
F;105-171/Domain: LIM domain 2 #status predicted <LD2>  
F;116-169/Domain: LIM metal-binding repeat homology <LIM>  
F;258-322/Domain: LIM metal-binding repeat homology <HOM>  
F;261-317/Domain: homeobox homology <HOX>  
  
Query Match 83.7%; Score 36; DB 2; Length 400;  
Best Local Similarity 71.4%; Pred. No. 21;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CEEDFYR 7  
Db 103 CKEDYR 109  
  
RESULT 6  
A47179  
homeotic protein LH-2 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Jul-1997  
C;Accession: A47179  
R;Xu, Y.; Baldassare, M.; Fisher, P.; Rathbun, G.; Oltz, E.M.; Yancopoulos, G.D.; Jesse  
Proc. Natl. Acad. Sci. U.S.A. 90, 227-231, 1993  
A;Title: LH-2: a LIM/homeodomain gene expressed in developing lymphocytes and neural ce

A;Reference number: A47179; MUID:93126348; PMID:7678338  
 A;Accession: A47179  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-426 <XU1>

A;Cross-references: GB:I06804  
 A;Experimental source: brain  
 A;Note: sequence inconsistent with the nucleotide translation  
 A;Note: sequence extracted from NCBI backbone (NCBIN:122101, NCBI:122102)  
 C;Superfamily: homeotic protein LH-2; homeobox homology; LIM metal-binding repeat homolog  
 C;Keywords: DNA binding; duplication; homeobox; nucleus; transcription regulation; zinc  
 F;52-104/Domain: LIM metal-binding repeat homology <LIM1>  
 F;114-167/Domain: LIM metal-binding repeat homology <LIM2>  
 F;265-321/Domain: homeobox homology <HOX>

Query Match 83.7%; Score 36; DB 1; Length 426;  
 Best Local Similarity 71.4%; Pred. No. 22;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7  
 |:|:|:  
 Db 101 CKEDYR 107

## RESULT 7

B86202  
 hypothetical protein [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C;Accession: B86202  
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federespiel, N.A.; Kaul, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: B86202  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-726 <STO>  
 A;Cross-references: GB:AE005172; NID:g7523705; PIDN:AAF63144.1; GSPDB:GN00141  
 C;Genetics:  
 A;Map position: 1

Query Match 83.7%; Score 36; DB 2; Length 726;  
 Best Local Similarity 85.7%; Pred. No. 38;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CEEDFYR 7  
 |:|:|:  
 Db 633 CEEDYR 639

## RESULT 8

B81371  
 hypothetical protein Cj0963 [imported] - Campylobacter jejuni (strain NCTC 11168)  
 C;Species: Campylobacter jejuni  
 C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002

C;Accession: B81371  
 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chillin  
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel  
 Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hvt

A;Reference number: A81250; MUID:20150912; PMID:10688204  
 A;Accession: B81371

A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-202 <PAR>

A;Cross-references: GB:AL139076; GB:AL111168; NID:g96968128; PIDN:CAB73220.1; PID:g969684  
 A;Experimental source: serotype O2, strain NCTC 11168  
 C;Genetics:  
 A;Gene: Cj0963

Query Match 81.4%; Score 35; DB 2; Length 202;  
 Best Local Similarity 83.3%; Pred. No. 17;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6  
 |:|:|:  
 Db 99 CEEDFY 104

## RESULT 9

AC0609  
 conserved hypothetical protein STY0935 [imported] - Salmonella enterica subsp. enterica  
 C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C;Accession: AC0609  
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
 th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
 S.; Moule, S.; O'Gaora, P.  
 Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero  
 A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AC0609  
 A;Status: preliminary

A;Molecule type: DNA  
 A;Residues: 1-552 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD05341.1; PID:g16502105; GSPDB:GN00176  
 C;Genetics:  
 A;Gene: STY0935

Query Match 81.4%; Score 35; DB 2; Length 552;  
 Best Local Similarity 71.4%; Pred. No. 45;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7  
 |:|:|:  
 Db 103 CEEDFYR 109

## RESULT 10

S63986

collagen alpha 5 chain - sea urchin (Strongylocentrotus purpuratus) (fragment)

C;Species: Strongylocentrotus purpuratus (purple urchin)

C;Date: 20-Jul-1996 #sequence\_revision 08-Nov-1996 #text\_change 25-Apr-1997

C;Accession: S63986; S64638  
 R;Exposito, J.Y.; Boute, N.; Deleage, G.; Garrone, R.

Eur. J. Biochem. 234, 59-65, 1995

A;Title: Characterization of two genes coding for a similar four-cysteine motif of the a

A;Reference number: S63985; MUID:96096722; PMID:8529669

A;Accession: S63986  
 A;Status: nucleic acid sequence not shown

A;Molecule type: DNA  
 A;Residues: 1-1376 <EXP>

A;Cross-references: EMBL:X89804  
 R;Exposito, J.Y.

submitted to the EMBL Data Library, July 1995

A;Reference number: S64637  
 A;Accession: S64638

A;Molecule type: DNA  
 A;Residues: 1-658, 'G', 660-870, 'G', 872-901, 'H', 903-1185, 'T', 1187-1214, 'Y', 1216-1376 <EXM>

A;Cross-references: EMBL:X89804  
 C;Genetics:

A;Gene: COLP5alpha

A;Introns: 73/1; 136/2; 221/1; 369/1; 517/1; 659/1; 799/1; 948/1; 1093/1; 1236/1

C;Superfamily: von Willebrand factor type C repeat homology

C;Keywords: extracellular matrix  
 F;15-73/Domain: von Willebrand factor type C repeat homology <VMC>

Query Match 81.4%; Score 35; DB 2; Length 1376;  
Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEEDFY 6  
|||||  
Db 1335 CEEDYY 1340

## RESULT 11

S63985  
collagen alpha 2 chain precursor - sea urchin (Strongylocentrotus purpuratus) (fragment)  
C:Species: Strongylocentrotus purpuratus (purple urchin)  
C:Date: 20-Jul-1996 #sequence\_revision 01-Nov-1996 #text\_change 15-Sep-2003  
C:Accession: S63985; S64637  
R:Exposito, J.Y.; Boute, N.; Deleage, G.; Garrone, R.  
Eur. J. Biochem. 234, 59-65, 1995  
A:Title: Characterization of two genes coding for a similar four-cysteine motif of the a  
A:Reference number: S63985; MUID:96096722; PMID:8529669  
A:Accession: S63985  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-1822 <EXP>  
A:Cross-references: EMBL:X89806  
R:Exposito, J.Y.  
submitted to the EMBL Data Library, July 1995  
A:Reference number: S64637  
A:Accession: S64637  
A:Molecule type: DNA  
A:Residues: 1-381,'DT',384-677,'N',679-1010,'L',1012-1822 <EXW>  
A:Cross-references: EMBL:X89806  
C:Genetics:  
A:Gene: COL2A1alpha  
A:Introns: 33/1; 106/1; 169/2; 254/1; 395/1; 460/3; 534/1; 678/1; 743/3 817/1; 965/1; 11  
F:48-106/Domain: von Willebrand factor type C repeat homology <VWC>

Query Match 81.4%; Score 35; DB 2; Length 1822;  
Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEEDFY 6  
|||||  
Db 1781 CEEDYY 1786

## RESULT 12

A43426  
collagen alpha 2 fibrillar chain precursor - sea urchin (Strongylocentrotus purpuratus)  
C:Species: Strongylocentrotus purpuratus (purple urchin)  
C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Sep-2003  
C:Accession: A43426  
R:Exposito, J.Y.; D'Alessio, M.; Ramirez, F.  
J. Biol. Chem. 267, 17404-17408, 1992  
A:Title: Novel amino-terminal propeptide configuration in a fibrillar procollagen underg  
A:Reference number: A43426; MUID:92381062; PMID:1380962  
A:Accession: A43426  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-3198 <EXP>  
A:Cross-references: GB:M92041; NID:gl51448; PIDN:AAA30040.1; PID:gl51449  
A:Note: sequence extracted from NCBI backbone (NCBIP:111965)  
F:48-106/Domain: von Willebrand factor type C repeat homology <VWC>  
F:2978-3198/Domain: fibrillar collagen carboxyl-terminal homology <FCC>

Query Match 81.4%; Score 35; DB 2; Length 3198;  
Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEEDFY 6  
|||||  
Db 1778 CEEDYY 1783

## RESULT 13

E84478  
hypothetical protein At2g06570 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: E84478  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.B.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: E84478  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-277 <STO>  
A:Cross-references: GB:AF002093; NID:g4584359; PIDN:AAD25153.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g06570  
A:Map position: 2

Query Match 79.1%; Score 34; DB 2; Length 277;  
Best Local Similarity 83.3%; Pred. No. 36;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEEDFY 6  
|||||  
Db 204 CEEDFF 209

## RESULT 14

E97111  
L-asparaginase [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
C:Accession: E97111  
R:Nalling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee  
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4836, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: E97111  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-331 <KUR>  
A:Cross-references: GB:AF001437; PIDN:AAK79680.1; PID:gl5024680; GSPDB:GN00168  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC1714  
C:Superfamily: asparaginase

Query Match 79.1%; Score 34; DB 2; Length 331;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 EEDFYR 7  
|||||  
Db 323 EEDFYR 328

## RESULT 15

AG2393  
DNA repair helicase [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
C:Accession: AG2393  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An  
A:Reference number: AB1807; MUID:21595285; PMID:11759640



A;Accession: AG2393  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-563 <KUR>  
 A;Cross-references: GB:BA000019; PIDN:BA076402.1; PID:gl7133840; GSPDB:GN00179  
 A;Experimental source: strain PCC 7120  
 C;Genetics:  
 A;Gene: alr4703

Query Match 79.1%; Score 34; DB 2; Length 563;  
 Best Local Similarity 85.7%; Pred. No. 72;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CEEDFYR 7  
 |||||  
 Db 531 CEEDFAR 537

Search completed: June 9, 2004, 15:52:18  
 Job time : 8.75676 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 9, 2004, 15:36:55 ; Search time 5.10811 Seconds  
(without alignments)  
71.355 Million cell updates/sec

Title: US-09-660-302D-7  
Perfect score: 43  
Sequence: 1 CEEDFYR 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	88.4	638	1	GHR_HUMAN
2	38	88.4	638	1	GHR_MACMU
3	37	86.0	399	1	CK05_MOUSE
4	36	83.7	20	1	UN05_FPNPS
5	36	83.7	364	1	MYCL_HUMAN
6	36	83.7	368	1	MYCL_MOUSE
7	36	83.7	388	1	LHX3_HUMAN
8	36	83.7	388	1	LHX3_MOUSE
9	36	83.7	406	1	LHX2_HUMAN
10	36	83.7	406	1	LHX2_MOUSE
11	36	83.7	426	1	LHX2_RAT
12	35	81.4	372	1	COLB_ARATH
13	34	79.1	599	1	CEL_MOUSE
14	34	79.1	612	1	CEL_RAT
15	34	79.1	707	1	NRDD_HABIN
16	34	79.1	737	1	AD02_RAT
17	33	76.7	86	1	Y576_ARCFU
18	33	76.7	272	1	ENGW_MYCPU
19	32	74.4	154	1	PYR1_BUCAL
20	32	74.4	367	1	LHX4_HUMAN
21	32	74.4	367	1	LHX4_MOUSE
22	32	74.4	373	1	FBLP_HUMAN
23	32	74.4	395	1	LHX3_CHICK
24	32	74.4	403	1	CK05_HUMAN
25	32	74.4	415	1	THD1_BACHD
26	32	74.4	486	1	HHIR_RAT
27	32	74.4	487	1	HHIR_HUMAN
28	32	74.4	487	1	HHIR_FANTR
29	32	74.4	488	1	HHIR_CAVPO
30	32	74.4	488	1	HHIR_MOUSE
31	32	74.4	491	1	HHIR_BOVIN
32	32	74.4	581	1	NET2_CHICK
33	32	74.4	604	1	NET1_MOUSE

34 32 74.4 606 1 NET1\_CHICK Q09222 gallus gall  
35 32 74.4 647 1 PEPO\_LACHE OS2071 lactobacill  
36 32 74.4 647 1 SK01\_YEAST Q02100 saccharomyc  
37 32 74.4 727 1 NETA\_DROME Q24567 drosophila  
38 32 74.4 796 1 COPP\_SCHPO Q42937 schizosacch  
39 32 74.4 976 1 EPA2\_HUMAN P29317 homo sapien  
40 32 74.4 1005 1 EPA5\_RAT P54757 rattus norv  
41 32 74.4 1037 1 EPA5\_HUMAN P54756 homo sapien  
42 32 74.4 1696 1 PKK5\_BRACL Q9nj15 branchiosto  
43 31 72.1 90 1 YHCO\_ECOLI P46480 escherichia  
44 31 72.1 148 1 PER2\_ARATH O04090 arabidopsis  
45 31 72.1 230 1 YGEA\_ECOLI P03813 escherichia

## ALIGNMENTS

## RESULT 1

GHR\_HUMAN  
ID GHR\_HUMAN STANDARD; PRT; 638 AA.  
AC P10912;  
DT 01-JUL-1989 (Rel. 11, Created)  
DT 01-JUL-1989 (Rel. 11, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Growth hormone receptor precursor (GH receptor) (Serum binding  
DE protein).  
DE GHR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=88065896; PubMed=2825030;  
RA Leung D.W., Spencer S.A., Cachianes G., Hammonds R.G., Collins C.,  
RA Henzel W.J., Barnard R., Waters M.J., Wood W.I.;  
RT "Growth hormone receptor and serum binding protein: purification,  
RT cloning and expression."  
RL Nature 330:537-543 (1987).  
RN [2]  
RP SEQUENCE FROM N.A., AND VARIANT LEU-544.  
RX MEDLINE=90046742; PubMed=2813379;  
RA Codowski P.J., Leung D.W., Meacham L.R., Galgani J.P., Hellmiss R.,  
RA Keret R., Rotwein P.S., Parks J.S., Larson Z., Wood W.I.;  
RT "Characterization of the human growth hormone receptor gene and  
RT demonstration of a partial gene deletion in two patients with Laron-  
RT type dwarfism."  
RL Proc. Natl. Acad. Sci. U.S.A. 86:8083-8087 (1989).  
RN [3]  
RP DISULFIDE BONDS.  
RX MEDLINE=90153957; PubMed=2406245;  
RA Fuh G., Mulkerin M.G., Bass S., McFarland N., Brochier M.,  
RA Bourrel J.H., Light D.R., Wells J.A.;  
RT "The human growth hormone receptor. Secretion from Escherichia coli  
RT and disulfide bonding pattern of the extracellular binding domain."  
RL J. Biol. Chem. 265:3111-3115 (1990).  
RN [4]  
RP VARIANT LARON DWARFISM SER-114.  
RX MEDLINE=89384829; PubMed=2779634;  
RA Amselem S., Duquesnoy P., Attree O., Novelli G., Bousnina S.,  
RA Postelvinay M.-C., Goossens M.;  
RT "Laron dwarfism and mutations of the growth hormone-receptor gene."  
RL New Engl. J. Med. 321:989-995 (1989).  
RN [5]  
RP VARIANTS LARON DWARFISM  
RX MEDLINE=93278381; PubMed=8504296;  
RA Amselem S., Duquesnoy P., Duriez B., Dastot F., Sorbier M.-L.,  
RA Vallex S., Goossens M.;  
RT "Spectrum of growth hormone receptor mutations and associated  
RT haplotypes in Laron syndrome."  
RL Hum. Mol. Genet. 2:355-359 (1993).  
RN [6]

RP VARIANT LARON DWARFISM HIS-170.  
 RX MEDLINE=94185645; PubMed=8137822;  
 RA Duesquesnoy P., Sobrier M.-L., Duriez B., Dastot F., Buchanan C.R.,  
 RA Savage M.O., Preece M.A., Craescu C.T., Plouquit Y., Goossens M.,  
 RA Anselm S.;  
 RT "A single amino acid substitution in the exoplasmic domain of the  
 RT human growth hormone (GH) receptor confers familial GH resistance  
 RT (Laron syndrome) with positive GH-binding activity by abolishing  
 RT receptor homodimerization.";  
 RL EMBO J. 13:1386-1395(1994).  
 [7]  
 RN VARIANTS IDIOPATHIC SHORT STATURE LYS-62; CYS-179 AND ASP-242.  
 RP MEDLINE=96013502; PubMed=7565946;  
 RX Goddard A.D., Covello R., Luoh S.-M., Clarkson T., Attie K.M.,  
 RA Gesundheit N., Rundle A.C., Wells J.A., Carlsson L.M.S.;  
 RT "Mutations of the growth hormone receptor in children with idiopathic  
 RT short stature.";  
 RL New Engl. J. Med. 333:1093-1098(1995).  
 [8]  
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 19-256.  
 RP MEDLINE=92196577; PubMed=1549776;  
 RX de Vos A.M., Uitsch M., Kossiakoff A.A.;  
 RA "Human growth hormone and extracellular domain of its receptor:  
 RT crystal structure of the complex.";  
 RL Science 255:306-312(1992).  
 [9]  
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 19-256.  
 RP MEDLINE=97113023; PubMed=8943276;  
 RX Sundstroem M., Lundqvist T., Roedien J., Giebel L.B., Milligan D.,  
 RA Norstedt G.;  
 RT "Crystal structure of an antagonist mutant of human growth hormone,  
 RT G120R, in complex with its receptor at 2.9-A resolution.";  
 RL J. Biol. Chem. 271:32197-32203(1996).  
 [10]  
 RN VARIANTS HIS-179; HIS-229; PHE-440; THR-495; LEU-544 AND THR-579.  
 RP MEDLINE=93318093; PubMed=10391209;  
 RX Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nimesh J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,  
 RA Lander E.S.;  
 RT "Characterization of single-nucleotide polymorphisms in coding regions  
 RT of human genes.";  
 RL Nat. Genet. 22:231-238(1999).  
 [11]  
 RN ERRATUM.  
 RP Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nimesh J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,  
 RA Lander E.S.;  
 RL Nat. Genet. 23:373-373(1999).  
 CC -!- FUNCTION: This is a receptor for pituitary gland growth hormone.  
 CC -!- SUBUNIT: Homodimer.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- DISEASE: Defects in GHR are a cause of Laron dwarfism  
 CC [MIM:262500]; also known as pituitary dwarfism II (Laron-type  
 CC pituitary dwarfism or Laron syndrome (LS)).  
 CC -!- DISEASE: Defects in GHR are a cause of idiopathic short stature  
 CC [MIM:600946].  
 CC -!- SIMILARITY: Belongs to the type I cytokine family of receptors.  
 CC Subfamily 1.  
 CC -!- SIMILARITY: Contains 1 fibronectin type III domain.  
 CC  
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 CC  
 CC -----  
 DR EMBL; X06562; CAA29808.1; -;  
 DR EMBL; M28466; AAA52555.1; -;  
 DR EMBL; M28458; AAA52555.1; JOINED.

DR EMBL; M28459; AAA52555.1; JOINED.  
 DR EMBL; M28460; AAA52555.1; JOINED.  
 DR EMBL; M28461; AAA52555.1; JOINED.  
 DR EMBL; M28462; AAA52555.1; JOINED.  
 DR EMBL; M28463; AAA52555.1; JOINED.  
 DR EMBL; M28464; AAA52555.1; JOINED.  
 DR EMBL; M28465; AAA52555.1; JOINED.  
 DR PIR; A33991; A33991.  
 DR PDB; 3HR; 30-APR-94.  
 DR PDB; 1HW; 19-NOV-97.  
 DR PDB; 1HW; 19-NOV-97.  
 DR PDB; 1AXI; 28-JAN-98.  
 DR PDB; 1A22; 29-APR-98.  
 DR PDB; 1KF9; 20-NOV-02.  
 DR Genew; HGNC:4263; GHR.  
 DR MIM; 600946; -;  
 DR MIM; 262500; -;  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR GO; GO:0004903; F:growth hormone receptor activity; TAS.  
 DR GO; GO:0007150; P:growth pattern; TAS.  
 DR GO; GO:0001501; P:skeletal development; TAS.  
 DR InterPro; IPR002996; CR1A.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR003528; Hemopoptn\_L\_Fl.  
 DR Pfam; PF00041; fn3; 1.  
 DR SMART; SMO0060; FN3; 1.  
 DR PROSITE; PS01352; HEMATOPO REC L Fl; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure;  
 KW Dwarfism; Polymorphism; Disease mutation.  
 KW SIGNAL 1  
 FT CHAIN 19 638 GROWTH HORMONE RECEPTOR.  
 FT DOMAIN 19 264 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 265 288 POTENTIAL.  
 FT DOMAIN 289 638 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 145 252 FIBRONECTIN TYPE-III.  
 FT DISULFID 56 66  
 FT DISULFID 101 112  
 FT DISULFID 126 140  
 FT CARBOHYD 46 46  
 FT CARBOHYD 115 115  
 FT CARBOHYD 156 156  
 FT CARBOHYD 161 161  
 FT CARBOHYD 200 200  
 FT VARIANT 62 62  
 FT VARIANT 89 89  
 FT VARIANT 114 114  
 FT VARIANT 143 143  
 FT VARIANT 162 162  
 FT VARIANT 170 170  
 FT VARIANT 179 179  
 FT VARIANT 179 179  
 FT VARIANT 229 229  
 FT VARIANT 229 229  
 FT VARIANT 242 242  
 FT VARIANT 440 440  
 FT VARIANT 495 495  
 FT VARIANT 544 544  
 FT  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 E -> K (in idiopathic short stature).  
 /FTid=VAR\_002708.  
 R -> K (in Laron dwarfism).  
 /FTid=VAR\_002709.  
 F -> S (in Laron dwarfism).  
 /FTid=VAR\_002710.  
 V -> A (in Laron dwarfism).  
 /FTid=VAR\_002711.  
 V -> D (in Laron dwarfism).  
 /FTid=VAR\_002712.  
 D -> H (in Laron dwarfism; abolish  
 receptor homodimerization).  
 /FTid=VAR\_002713.  
 R -> C (in Laron dwarfism and idiopathic  
 short stature).  
 /FTid=VAR\_002714.  
 R -> H (in dbSNP:6181).  
 /FTid=VAR\_013937.  
 R -> G (in Laron dwarfism).  
 /FTid=VAR\_002715.  
 R -> H (in dbSNP:6177).  
 /FTid=VAR\_013938.  
 E -> D (in idiopathic short stature).  
 /FTid=VAR\_002716.  
 C -> F (in dbSNP:6182).  
 /FTid=VAR\_013939.  
 P -> T (in dbSNP:6183).  
 /FTid=VAR\_013940.  
 I -> L (in dbSNP:6180).  
 /FTid=VAR\_013941.

259 CEEDFY 264

DB

RESULT 3

CK05\_MOUSE

ID CK05\_MOUSE STANDARD; PRT; 399 AA.

AC Q9QY66;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Protein Cllor5f5 homolog (Protein FON).

DE Cllor5f5.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

EX MEDLINE=20069078; PubMed=10602999;

RA Lemmens I.H., Farnbo F., Piehl F., Merregaert J., Van de Ven W.J.M.,

RA Larsson C., Kas K.

RT "Molecular characterization of human and murine cllor5f5, a new member

RT of the FAUNA gene cluster.";

RL Mamm. Genome 11:78-80(2000).

CC -!- TISSUE SPECIFICITY: low expression in most tissues; highly

CC expressed in testis; particularly in seminiferous tubules.

CC -----

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CC -----

CC EMBL; AF119498; AAF23592.1; -.

DR MGD; MGI:1352481; ORF6.

DR InterPro; IPR007529; Znf HIT.

DR Pfam; PF04438; zf-HIT; 1.

SO SEQUENCE 399 AA; 43038 MW; 6BED852632747B54 CRC64;

Query Match 86.0%; Score 37; DB 1; Length 399;

Best local Similarity 85.7%; Pred. No. 7.7;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CEEDFYR 7

DB 41 CAEDFYR 47

|||||

|||||

RESULT 4

UN05\_PINPS

ID UN05\_PINPS STANDARD; PRT; 20 AA.

AC P81674;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Unknown protein from 2D-page of needles (N147) (Fragments).

OS Pinus pinaster (Maritime pine).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.

OX NCBI\_TaxID=17647;

RN [1]

RP SEQUENCE.

RC TISSUE=Needle;

RX MEDLINE=99274088; PubMed=10344291;

RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,

RA Frigerio J.-M., Plomion C.

RT "Separation and characterization of needle and xylem maritime pine

RT proteins.";

RL Electrophoresis 20:1098-1108(1999).

CC -!- MISCELLANEOUS: On the 2-gel the determined pI of this unknown

CC protein is 5.6, its MW is 36 kDa.

```

FT NON_TER 1 1
FT NON_CONS 11 12
FT VARIANT 13 13 F -> I.
FT VARIANT 14 14 Y -> E.
FT VARIANT 15 15 R -> K.
FT NON_TER 20 20
FT SEQUENCE 20 AA; 2438 MW; 9FAE4678E086C298 CRC64;

Query Match 83.7%; Score 36; DB 1; Length 20;
Best Local Similarity 71.4%; Pred. No. 0.51;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
|::|||
Db 9 CDKDFYR 15

RESULT 5
MYCL_HUMAN STANDARD; PRT; 364 AA.
ID MYCL_HUMAN Q9NUE9;
AC P12524;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE L-myc-1 proto-oncogene protein.
DE MYCL1 OR MYCL OR LMYC.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88094386; PubMed=2827002;
RA Kaye F., Battey J., Nau M., Brooks B., Seifter E., de Greve J.,
RA Barrer M., Sausville E., Minna J.;
RT "Structure and expression of the human L-myc gene reveal a complex
RT pattern of alternative mRNA processing.";
RL Mol. Cell. Biol. 8:186-195(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88112807; PubMed=3322939;
RA Depinho R.A., Hatton K.S., Testfave A., Yancopoulos G.D., Alt F.W.;
RT "The human myc gene family: structure and activity of L-myc and an
RT L-myc pseudogene.";
RL Genes Dev. 1:1311-1326(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX Ellington A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBUNIT: Efficient DNA binding requires dimerization with another
CC BHLH protein. Binds DNA as an heterodimer with MAX.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC
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CC
CC EMBL; M19720; AAA59879.1; -
CC EMBL; X07262; CAA30248.1; -
CC EMBL; X07263; CAA30249.1; -
CC EMBL; AL033527; CAB75682.1; -
CC PIR; A27675; TVHML.
CC HSP; P25912; 1HLO.
CC TRANSFAC; T02385; -
CC Genew; HGNC:7555; MYCL1.
CC MIM; 164850; -
CC GO; GO:0003677; F:DNA binding; NAS.
CC InterPro; IPR001092; HLH_basic.

```

```

DR InterPro; IPR002418; TF_Myc.
DR Pfam; PF001010; HLH; 1.
DR Pfam; PF01056; MYC_N term; 1.
DR PRINTS; PR00044; LEUZIPPRMYC.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PS00888; HLH; 1.
KW Nuclear protein; DNA-binding; Proto-oncogene.
FT DNA BIND 282 294 BASIC DOMAIN.
FT DOMAIN 295 334 HELIX-LOOP-HELIX MOTIF.
FT DOMAIN 333 361 LEUCINE-ZIPPER (POTENTIAL).
FT CONFLICT 362 362 S -> T (IN REF. 3).
SQ SEQUENCE 364 AA; 40312 MW; 58F8A71A1C2ED6D4 CRC64;

Query Match 83.7%; Score 36; DB 1; Length 364;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
|::|||
Db 15 CGEDFYR 21

RESULT 6
MYCL_MOUSE STANDARD; PRT; 368 AA.
ID MYCL_MOUSE P10166;
AC P10166;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE L-myc proto-oncogene protein.
DE MYCL1 OR MYCL OR LMYC1.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c;
RX MEDLINE=88111523; PubMed=2828024;
RA Legouy E., Depinho R.A., Zimmerman K., Collum R., Yancopoulos G.D.,
RA Mitsock L., Kriz R., Alt F.W.;
RT "Structure and expression of the murine L-myc gene.";
RL EMBO J. 6:3359-3366(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBUNIT: Efficient DNA binding requires dimerization with another
CC BHLH protein. Binds DNA as an heterodimer with MAX.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
CC
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CC -----  
 DR EMBL; X13945; CAA32128.1; -;  
 DR EMBL; BC053059; AAH53059.1; -;  
 DR PIR; S03017; TWMSM.  
 DR HSP; P25912; IHLO.  
 DR TRANSFAC; T02387; -;  
 DR MGD; MGI:96799; Lmycl.  
 DR InterPro; IPR001092; HLH basic.  
 DR InterPro; IPR002418; TF\_Myc.  
 DR Pfam; PF00010; HLH; 1; Myc.  
 DR Pfam; PF01056; Myc\_N\_term; 1.  
 DR PRINTS; PR00044; LEUZIPPRMYC.  
 DR SMART; SM00353; HLH; 1.  
 DR PROSITE; PS00888; HLH; 1.  
 DR Nuclear protein; DNA-binding; Proto-oncogene.  
 FT DNA\_BIND 286 298 BASIC DOMAIN  
 FT DOMAIN 299 338 HELIX-LOOP-HELIX MOTIF.  
 FT DOMAIN 337 365 LEUCINE-ZIPPER (POTENTIAL).  
 SQ SEQUENCE 368 AA; 40848 MW; 9174F6FD7C03321E CRC64;

Query Match 83.7%; Score 36; DB 1; Length 368;  
 Best Local Similarity 85.7%; Pred.No. 11;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CEEDFYR 7  
 | | | | |  
 DB 15 CGEDFYR 21

## RESULT 7

LHX9\_HUMAN  
 ID LHX9\_HUMAN STANDARD; PRT; 388 AA.  
 AC Q9N0G9; Q9BYU6; Q9NQ70;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE LIM/homeobox protein Lhx9.  
 GN LHX9.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=21291005; PubMed=11397841;  
 RA Ottolenghi C., Moreira-Filho C., Mendonca B.B., Barbieri M.,  
 RA Fellous M., Berkovitz G.D., McElreavey K.;  
 RT "Absence of mutations involving the LIM homeobox domain gene LHX9 in  
 RT 46,Xy gonadal agenesis and dysgenesis.";  
 RL J. Clin. Endocrinol. Metab. 86:2465-2469(2001).  
 CC -!- FUNCTION: Involved in gonadal development (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -!- SIMILARITY: Contains 1 homeobox domain.  
 CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.  
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DR EMBL; AJ277915; CAB97493.1; -;  
 DR EMBL; AJ277916; CAB98128.1; ALT SEQ.  
 DR EMBL; AJ277917; CAB98128.1; JOINED.

DR EMBL; AJ277918; CAB98128.1; JOINED.  
 DR EMBL; AJ277919; CAB98128.1; JOINED.  
 DR EMBL; AJ277920; CAB98128.1; JOINED.  
 DR EMBL; AJ296272; CAC33174.1; -;  
 DR HSP; P06601; 1FJL.  
 DR Genew; HGNC:14222; LHX9.  
 DR MIM; 606066; -;  
 DR InterPro; IPR001356; Homeobox.  
 DR InterPro; IPR001781; LIM.  
 DR InterPro; IPR007107; LIM\_homeo.  
 DR Pfam; PF00046; homeobox; 1.  
 DR Pfam; PF00412; LIM; 2.  
 DR ProDom; PD000010; Homeobox; 1.  
 DR ProDom; PD000094; LIM; 2.  
 DR SMART; SM00389; HOK; 1.  
 DR SMART; SM00132; LIM; 2.  
 DR PROSITE; PS00478; LIM\_DOMAIN\_1; 2.  
 DR PROSITE; PS00023; LIM\_DOMAIN\_2; 2.  
 DR PROSITE; PS00027; HOMEBOX\_1; 1.  
 DR PROSITE; PS00071; HOMEBOX\_2; 1.  
 KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;  
 KW Metal-binding; Zinc.  
 FT DOMAIN 62 114 LIM 1.  
 FT DOMAIN 124 177 LIM 2.  
 FT DNA\_BIND 258 317 HOMEBOX.  
 SQ SEQUENCE 388 AA; 42903 MW; A4DC8B914D7C3B66 CRC64;

Query Match 83.7%; Score 36; DB 1; Length 388;  
 Best Local Similarity 71.4%; Pred.No. 12;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7  
 | | | | |  
 DB 111 CREDFYR 117

## RESULT 8

LHX9\_MOUSE  
 ID LHX9\_MOUSE STANDARD; PRT; 388 AA.  
 AC Q9WHH2; Q9QYQ5; Q9QYQ6; Q9Q200; Q9WU44;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE LIM/homeobox protein Lhx9.  
 GN LHX9.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE OF 1-300 FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=99098964; PubMed=9880598;  
 RA Retaux S., Rogard M., Bach I., Failli V., Beason M.J.;  
 RT "Lhx9: a novel LIM-homeodomain gene expressed in the developing  
 RT forebrain.";  
 RL J. Neurosci. 19:783-793(1999).  
 RN [2]  
 RP SEQUENCE OF 11-388 FROM N.A.  
 RC STRAIN=NIH Swiss;  
 RX MEDLINE=99264291; PubMed=10330499;  
 RA Bertuzzi S., Porter F.D., Pitts A., Kumar M., Agulnick A., Wassif C.,  
 RA Westphal H.;  
 RT "Characterization of Lhx9, a novel LIM/homeobox gene expressed by the  
 RT pioneer neurons in the mouse cerebral cortex.";  
 RL Mech. Dev. 81:193-198(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC STRAIN=C57BL/6; TISSUE=Brain;  
 RX MEDLINE=2021375; PubMed=10756098;  
 RA Failli V., Rogard M., Mattei M.-G., Vernier P., Retaux S.;  
 RT "Lhx9 and Lhx9alpha LIM-homeodomain factors: genomic structure,  
 RT expression patterns, chromosomal localization, and phylogenetic





DR PROSITE; PS00478; LIM DOMAIN 1; 2.  
DR PROSITE; PS00023; LIM DOMAIN 2; 2.  
DR PROSITE; PS00027; HOMEBOX 1; 1.  
DR PROSITE; PS00071; HOMEBOX 2; 1.  
KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;  
Metal-binding; Zinc; Transcription regulation.  
FT DOMAIN 53 105 LIM 1.  
FT DOMAIN 115 168 LIM 2.  
FT DOMAIN 187 196 POLY-ALA.  
FT DNA BIND 266 325 HOMEBOX.  
FT DOMAIN 307 323 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
FT CONFLICT 22 28 AKSEAPA -> QERGR (IN REF. 1).  
FT CONFLICT 54 54 A -> G (IN REF. 1).  
FT CONFLICT 107 107 Y -> YPSLHGVP (IN REF. 2).  
FT CONFLICT 187 187 A -> Q (IN REF. 1).  
FT CONFLICT 190 192 AAA -> RAR (IN REF. 1).  
FT CONFLICT 196 196 MISSING (IN REF. 1).  
FT CONFLICT 241 242 NA -> TR (IN REF. 1).  
FT CONFLICT 391 406 GHPHSPSQTLTNLF -> AMSLTAPHKRLLTFSNDSQP  
PHTISLKXKLSLV (IN REF. 1).  
SQ SEQUENCE 406 AA; 44373 MW; DF73AAC81867D30D CRC64;

Query Match 83.7%; Score 36; DB 1; Length 406;  
Best Local Similarity 71.4%; Pred. No. 12;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7  
|:|:|:|  
DB 102 CKEDYR 108

RESULT 10  
LHX2 MOUSE  
ID LHX2 MOUSE STANDARD; PRT; 406 AA.  
AC Q9Z0S2;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE LIM/homeobox protein Lhx2.  
GN LHX2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99162575; PubMed=10051612;  
RA Rincon-Limas D.E., Lu C.-H., Canal I., Calleja M.,  
Rodriguez-Esteban C., Izpisua-Belmonte J.-C., Botas J.;  
RT "Conservation of the expression and function of apterous orthologs in  
Drosophila and mammals.";  
RL Proc. Natl. Acad. Sci. U.S.A. 96:2165-2170(1999).  
CC -!- FUNCTION: Transcriptional regulatory protein involved in the  
control of cell differentiation in developing lymphoid and neural  
cell types (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).  
CC -!- SIMILARITY: Contains 1 homeobox domain.  
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.  
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CC EMBL; AF124734; AAD20012.1; --  
CC HSSP; P06601; 1FJL.  
CC TRANSFAC; T01969; --  
CC MGD; MGI:96785; Lhx2.  
CC GO; GO:0007498; P:mesoderm development; IMP.  
CC GO; GO:0007399; P:neurogenesis; IMP.

DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR001781; LIM.  
DR InterPro; IPR007107; LIM homeo.  
DR Pfam; PF00046; homeobox; 1.  
DR Pfam; PF00412; LIM; 2.  
DR ProDom; PD000010; Homeobox; 1.  
DR ProDom; PD000094; LIM; 2.  
DR SMART; SM00389; HOX; 1.  
DR SMART; SM00132; LIM; 2.  
DR PROSITE; PS00478; LIM DOMAIN 1; 2.  
DR PROSITE; PS00023; LIM DOMAIN 2; 2.  
DR PROSITE; PS00027; HOMEBOX 1; 1.  
DR PROSITE; PS00071; HOMEBOX 2; 1.  
KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;  
Metal-binding; Zinc; Transcription regulation.  
FT DOMAIN 53 105 LIM 1.  
FT DOMAIN 115 168 LIM 2.  
FT DOMAIN 187 196 POLY-ALA.  
FT DNA BIND 266 325 HOMEBOX.  
FT DOMAIN 307 323 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
SQ SEQUENCE 406 AA; 44419 MW; FE7B4E76454D6A90 CRC64;

Query Match 83.7%; Score 36; DB 1; Length 406;  
Best Local Similarity 71.4%; Pred. No. 12;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7  
|:|:|:|  
DB 102 CKEDYR 108

RESULT 11  
LHX2 RAT  
ID LHX2 RAT STANDARD; PRT; 426 AA.  
AC P36198;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE LIM/homeobox protein Lhx2 (Homeobox protein Lhx-2).  
GN LHX2 OR LHX2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93126348; PubMed=7678338;  
RA Xu Y., Baldassare M., Fisher P., Rathbun G., Oltz E.M.,  
Yancopoulos G.D., Jessell T.M., Alt F.W.;  
RT "Lhx-2: a LIM/homeobox domain gene expressed in developing lymphocytes and  
neural cells.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:227-231(1993).  
CC -!- FUNCTION: Transcriptional regulatory protein involved in the  
control of cell differentiation in developing lymphoid and neural  
cell types.  
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).  
CC -!- TISSUE SPECIFICITY: Found in discrete regions of the developing  
CNS, primarily in diencephalic and telencephalic structures and  
a subset of lymphoid tissues. Also found in embryonic spinal chord  
and fetal liver.  
CC -!- DEVELOPMENTAL STAGE: Expressed in developing lymphocytes and  
neural cells. Maximal expression is found in pre-B-lymphocytes.  
CC -!- SIMILARITY: Contains 1 homeobox domain.  
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.  
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CC -----
DR EMBL: L06804; -; NOT_ANNOTATED_CDS.
DR HSP: P06601; 1FJL.
DR TRANSFAC; T01966; -.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR007107; LIM_homeo.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00478; LIM_DOMAIN 1; 2.
DR PROSITE; PS00023; LIM_DOMAIN 2; 2.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM domain;
KW Metal-binding; Zinc; Transcription regulation.
FT DOMAIN 52 104 LIM 1.
FT DOMAIN 114 167 LIM 2.
FT DNA_BIND 264 323 HOMEBOX.
FT DOMAIN 305 321 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 426 AA; 47418 MW; DC8FA3DB4572BB40 CRC64;

Query Match 83.7%; Score 36; DB 1; Length 426;
Best Local Similarity 71.4%; Pred. No. 13;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEDDFYR 7
Db 101 CKEDYR 107

RESULT 12
COLB ARATH
ID COLB ARATH STANDARD; PRT; 372 AA.
AC Q9SSE5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Zinc finger protein constans-like 11.
GN AT3G07650 OR MLP3.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unseld M.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Delany M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choiane N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erffle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Bauges M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Ilauro C., Fumelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Cready T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Millscher J., Sellers P., Gill J.B., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,

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RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Ideawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shingo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.,
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:820-822(2000).
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: Belongs to the CONSTANS family.
CC -!- SIMILARITY: Contains 2 B box-type zinc fingers.
CC -----
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CC -----
CC EMBL: AC009176; AAP13083.1; -.
DR InterPro; IPR000315; Znf_Bbox.
DR InterPro; IPR002926; Znf_Constans.
DR Pfam; PF00643; zf-B_box; 2.
DR ProDom; PD007661; Znf_constans; 1.
DR SMART; SM00336; BBOX; 2.
DR PROSITE; PS0119; ZF_BBOX; 2.
KW Zinc-finger; Nuclear protein; Repeat; Multigene family.
FT ZN_FING 5 47 B_BOX-TYPE 1.
FT ZN_FING 48 99 B_BOX-TYPE 2 (ATYPICAL).
FT DOMAIN 77 83 POLY-ASN.
FT DOMAIN 84 90 POLY-SER.
SQ SEQUENCE 372 AA; 40754 MW; 188F18B283D7479 CRC64;

Query Match 81.4%; Score 35; DB 1; Length 372;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEDDFY 6
Db 181 CEDDFY 186

RESULT 13
CEL_MOUSE
ID CEL_MOUSE STANDARD; PRT; 599 AA.
AC Q4285;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Bile-salt-activated lipase precursor (EC 3.1.1.3) (BAL)
DE (Bile-salt-stimulated lipase) (BSSL) (Carboxyl ester lipase) (Sterol
DE esterase) (cholesterol esterase) (pancreatic lysophospholipase).
GN CEL OR Lip1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Mammary gland;
RX MEDLINE=96096531; PubMed=8522186;
RA Mackay K., Lawn R.M.;
OC NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Lactating mammary gland;
RX MEDLINE=96079098; PubMed=8530060;
RA Lidmer A.S., Kannius M., Lundberg L., Bjursell G., Nilsson J.;
KW Molecular cloning and characterization of the mouse carboxyl ester
RT lipase gene and evidence for expression in the lactating mammary

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RT gland.";  
 CC Genomics 29:115-122(1995).  
 CC -!- FUNCTION: CATALYZES FAT AND VITAMIN ABSORPTION. ACTS IN CONCERT  
 CC WITH PANCREATIC LIPASE AND COLIPASE FOR THE COMPLETE DIGESTION  
 CC OF DIETARY TRIGLYCERIDES (BY SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a  
 CC fatty acid anion.  
 CC -!- CATALYTIC ACTIVITY: A sterol + H(2)O = a sterol + a fatty  
 CC acid.  
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U33169; AAA92088.1; -;  
 DR EMBL; U37386; AAC52279.1; -;  
 DR PIR; A57701; A57701.  
 DR HGSP; P30122; 2BCE.  
 DR SWISS-2DPAGE; Q64285; MOUSE.  
 DR MGD; MGI:88374; Cel.  
 DR GO; GO:0046514; P:ceramide catabolism; IMP.  
 DR InterPro; IPR002018; CarboxylesteraseB.  
 DR InterPro; IPR000379; Ser\_estr.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolase; Serine esterase; Lipid degradation; Glycoprotein;  
 KW Repeat; Signal.  
 FT SIGNAL 1 20 BY SIMILARITY.  
 FT CHAIN 21 599 BILE-SALT-ACTIVATED LIPASE.  
 FT ACT\_SITE 214 214 BY SIMILARITY.  
 FT ACT\_SITE 340 340 BY SIMILARITY.  
 FT ACT\_SITE 455 455 BY SIMILARITY.  
 FT DISULFID 84 100 BY SIMILARITY.  
 FT DISULFID 266 277 BY SIMILARITY.  
 FT DOMAIN 559 588 4 X 11 AA TANDEM REPEATS, O-GLYCOSYLATED  
 FT REPEAT 559 569 1.  
 FT REPEAT 570 580 2.  
 FT REPEAT 581 588 3.  
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 599 AA; 65813 MW; 9E4428FDFCA8602E CRC64;  
 Query Match 79.1%; Score 34; DB 1; Length 599;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 REDFYR 7  
 Db 361 EDFYR 366  
 RESULT 14  
 CEL\_RAT  
 ID CEL\_RAT STANDARD; PRT; 612 AA.  
 AC P07882; P14722;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Bile-salt-activated lipase precursor (EC 3.1.1.3) (BAL)  
 DE (Bile-salt-stimulated lipase) (BSSL) (Carboxyl ester lipase) (Sterol  
 DE esterase) (Cholesterol esterase) (Pancreatic lysophospholipase).  
 GN CEL.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid=10116;

[1] SEQUENCE FROM N.A.  
 RP STRAIN=Sprague-Dawley; TISSUE=Pancreas;  
 RX MEDLINE=90089378; PubMed=2688744;  
 RA Kissel J.A., Fontaine R.N., Turck C.W., Brockman H.L., Hui D.Y.;  
 RT "Molecular cloning and expression of cDNA for rat pancreatic  
 RT cholesterol esterase.",  
 RL Biochim. Biophys. Acta 1006:227-237(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87242339; PubMed=3593682;  
 RA Han J.H., Stratawa C., Rutter W.J.;  
 RT "Isolation of full-length putative rat lysophospholipase cDNA using  
 RT improved methods for mRNA isolation and cDNA cloning.",  
 RL Biochemistry 26:1617-1625(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91299758; PubMed=2069957;  
 RA Fontaine R.N., Carter C.P., Hui D.Y.;  
 RT "Structure of the rat pancreatic cholesterol esterase gene.",  
 RL Biochemistry 30:7008-7014(1991).  
 RN [4]  
 RP ACTIVE SITE SER-214.  
 RX MEDLINE=91009095; PubMed=2211595;  
 RA Dipersio L.P., Fontaine R.N., Hui D.Y.;  
 RT "Identification of the active site serine in pancreatic cholesterol  
 RT esterase by chemical modification and site-specific mutagenesis.",  
 RL J. Biol. Chem. 265:16801-16806(1990).  
 RN [5]  
 RP ACTIVE SITE HIS-455.  
 RX MEDLINE=91154187; PubMed=1993999;  
 RA Dipersio L.P., Fontaine R.N., Hui D.Y.;  
 RT "Site-specific mutagenesis of an essential histidine residue in  
 RT pancreatic cholesterol esterase.",  
 RL J. Biol. Chem. 266:4033-4036(1991).  
 CC -!- FUNCTION: CATALYZES FAT AND VITAMIN ABSORPTION. ACTS IN CONCERT  
 CC WITH PANCREATIC LIPASE AND COLIPASE FOR THE COMPLETE DIGESTION  
 CC OF DIETARY TRIGLYCERIDES.  
 CC -!- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a  
 CC fatty acid anion.  
 CC -!- CATALYTIC ACTIVITY: A sterol + H(2)O = a sterol + a fatty  
 CC acid.  
 CC -!- ENZYME REGULATION: Activated by bile salts containing a 7-hydroxyl  
 CC group.  
 CC -!- TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE PANCREAS AND THEN  
 CC TRANSPORTED TO THE INTESTINE.  
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC -----  
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 CC -----  
 DR EMBL; X16054; CAA34189.1; -;  
 DR EMBL; M15893; AAA41540.1; -;  
 DR EMBL; M6157; AAB46376.1; -;  
 DR PIR; A34967; A34967.  
 DR HGSP; P30122; 2BCE.  
 DR InterPro; IPR002018; CarboxylesteraseB.  
 DR InterPro; IPR000379; Ser\_estr.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolase; Serine esterase; Lipid degradation; Glycoprotein;  
 KW Repeat; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 612 BILE-SALT-ACTIVATED LIPASE.  
 FT ACT\_SITE 214 214  
 FT ACT\_SITE 340 340 BY SIMILARITY.  
 FT ACT\_SITE 455 455

FT DISULFID 84 100 BY SIMILARITY.  
FT DISULFID 266 277 BY SIMILARITY.  
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT DOMAIN 556 599 4 X 11 AA TANDEM REPEATS, O-GLYCOSYLATED REGION.  
FT REPEAT 556 566 1.  
FT REPEAT 567 577 2.  
FT REPEAT 578 588 3.  
FT REPEAT 589 599 4.  
FT MUTAGEN 440 440 H->Q,R,A,S,D: ABOLISHES ACTIVITY.  
FT MUTAGEN 455 455 V -> L (IN REF. 2).  
FT CONFLICT 26 26 G -> A (IN REF. 2).  
FT CONFLICT 154 154 A -> G (IN REF. 2).  
FT CONFLICT 217 217 S -> I (IN REF. 2).  
FT CONFLICT 219 219 M -> T (IN REF. 3).  
FT CONFLICT 419 419 T -> M (IN REF. 2 AND 3).  
FT CONFLICT 513 513 GG -> VV (IN REF. 3).  
FT CONFLICT 576 577 GP -> VA (IN REF. 3).  
FT CONFLICT 608 609 G -> A (IN REF. 3).  
FT CONFLICT 611 611  
SQ SEQUENCE 612 AA; 67040 MW; 1569CE4EA71ED02A CRC64;  
  
Query Match 79.1%; Score 34; DB 1; Length 612;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 EEDFYR 7  
| | | | |  
Db 361 EEDFYR 366  
  
RESULT 15  
NRDD HAEIN STANDARD; PRT; 707 AA.  
AC P43752;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2).  
GN NRDD OR HI0075.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Haemophilus.  
OX NCBI\_TaxID=727;  
[1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=Rd / KW20 / ATCC 51907;  
RX MEDLINE=95350630; PubMed=7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Cotton M.D.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Brandon R.C.,  
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brannon R.C.,  
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae  
Rd.";  
RL Science 269:496-512(1995).  
CC -!- CATALYTIC ACTIVITY: 2'-deoxyribonucleoside triphosphate + oxidized  
CC thioredoxin + H(2)O = ribonucleoside triphosphate + reduced  
CC thioredoxin.  
CC -!- SUBUNIT: Tetramer consisting of 2 alpha (Nrdd) and 2 beta (NrDG)  
CC subunits (By similarity).  
CC -!- SIMILARITY: STRONG, TO E.COLI AND T4 NRDD.  
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CC -----  
DR EMBL; U32693; AAC21751.1; -.  
DR EIR; A64047; A64047.  
DR HSP; P07071; 1B8B.  
DR TIGR; HI0075; -.  
DR InterPro; IPR005144; ATP.  
DR InterPro; IPR001150; Form\_actrans\_GR.  
DR Pfam; PF03477; ATP-cone; 1.  
DR Pfam; PF01228; Gly radical; 1.  
DR PROSITE; PS00850; GLY\_RADICAL; 1. Complete proteome.  
KW Oxidoreductase; Organic radical; FREE RADICAL (BY SIMILARITY).  
FT MOD\_RES 682 682 FREE RADICAL (BY SIMILARITY).  
SQ SEQUENCE 707 AA; 80233 MW; A3795F7921A6781D CRC64;  
  
Query Match 79.1%; Score 34; DB 1; Length 707;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 EEDFYR 7  
| | | | |  
Db 425 EEDFYR 430  
  
Search completed: June 9, 2004, 15:49:06  
Job time : 6.10811 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 9, 2004, 15:43:00 ; Search time 23.4595 seconds  
(without alignments)  
94.147 Million cell updates/sec

Title: US-09-660-302D-7  
Perfect score: 43  
Sequence: 1 CEEDFYR 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	38	88.4	153	16	Q8R8G6	Q8R8G6 thermoanaer
2	38	88.4	632	6	Q95ML5	Q95ML5 salmieri bol
3	38	88.4	538	6	Q9XSZ1	Q9XSZ1 papio anubi
4	37	86.0	399	11	Q8VCQ7	Q8VCQ7 mus musculus
5	37	86.0	399	11	Q8C356	Q8C356 mus musculus
6	36	83.7	76	5	Q9U9B1	Q9U9B1 ancylostoma
7	36	83.7	91	5	Q16938	Q16938 ancylostoma
8	36	83.7	125	13	Q98SF6	Q98SF6 xenopus lae
9	36	83.7	206	4	Q14897	Q14897 homo sapien
10	36	83.7	325	13	Q98SF7	Q98SF7 xenopus lae
11	36	83.7	325	11	Q811Z4	Q811Z4 rattus norv
12	36	83.7	369	6	Q865X9	Q865X9 sus scrofa
13	36	83.7	378	13	Q90881	Q90881 gallus gall
14	36	83.7	388	11	Q80W90	Q80W90 rattus norv
15	36	83.7	397	4	Q86UH2	Q86UH2 homo sapien
16	36	83.7	400	13	O42108	O42108 gallus gall

17	36	83.7	726	10	Q9M9Y2	Q9M9Y2 arabidopsis
18	35	81.4	202	16	Q9PMX2	Q9PMX2 campylobact
19	35	81.4	219	10	Q8S056	Q8S056 oryza sativ
20	35	81.4	552	16	Q8ZQE6	Q8ZQE6 salmonella
21	35	81.4	552	16	Q8Z827	Q8Z827 salmonella
22	35	81.4	1376	5	Q26637	Q26637 strongyloce
23	35	81.4	1823	5	Q26638	Q26638 paracentrot
24	35	81.4	3198	5	Q26639	Q26639 strongyloce
25	34	79.1	102	16	Q8DZ48	Q8DZ48 streptococc
26	34	79.1	179	12	Q8JRV2	Q8JRV2 phthorimaea
27	34	79.1	182	5	Q815K6	Q815K6 plasmodium
28	34	79.1	262	5	Q8SU06	Q8SU06 encephalito
29	34	79.1	277	10	Q9SK11	Q9SK11 arabidopsis
30	34	79.1	331	16	Q97ID4	Q97ID4 clostridium
31	34	79.1	420	16	Q8RA45	Q8RA45 thermoanaer
32	34	79.1	457	16	Q7ML30	Q7ML30 bordetella
33	34	79.1	457	16	Q7W7P2	Q7W7P2 bordetella
34	34	79.1	457	16	Q7VV94	Q7VV94 bordetella
35	34	79.1	563	16	Q8YN67	Q8YN67 anabaena sp
36	34	79.1	592	11	Q64571	Q64571 rattus norv
37	34	79.1	599	11	Q922R3	Q922R3 mus musculu
38	34	79.1	625	3	O94300	O94300 schizosacch
39	34	79.1	1007	12	Q9QH62	Q9QH62 gallid herp
40	34	79.1	1256	5	Q81575	Q81575 plasmodium
41	34	79.1	1446	5	Q81DQ5	Q81DQ5 plasmodium
42	34	79.1	1595	4	Q81VG6	Q81VG6 homo sapien
43	33	76.7	98	5	Q16939	Q16939 ancylostoma
44	33	76.7	141	16	Q8DF30	Q8DF30 vibrio vuln
45	33	76.7	159	5	Q9W4Q9	Q9W4Q9 drosophila

## ALIGNMENTS

RESULT 1

Q8R8G6 ID Q8R8G6 PRELIMINARY; PRT; 153 AA.  
AC Q8R8G6  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Hypothetical protein TTE2033.  
GN TTE2033.  
OS Thermoanaerobacter tengcongensis.  
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;  
OC Thermoanaerobacteriaceae; Thermoanaerobacter.  
OX NCBI\_TaxID=119072;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MB4 / JCM 11007;  
RX MEDLINE=21992816; PubMed=11997336;  
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,  
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,  
Tan H., Chen R., Wang J., Yu J., Yang H.;  
RT "A complete sequence of T. tengcongensis genome.";  
RL Genome Res. 12:689-700(2002).  
DR EMBL; AF013153; AAM25210.1; --  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 153 AA; 18428 MW; 3B0F4ED430B1A0FA CRC64;

Query Match 88.4%; Score 38; DB 16; Length 153;  
Best Local Similarity 100.0%; Pred. No. 7.8;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFY 6

Db 21 CEEDFY 26

RESULT 2

Q95ML5 ID Q95ML5 PRELIMINARY; PRT; 632 AA.  
AC Q95ML5;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Growth hormone receptor.  
 OS Saimiri boliviensis (Bolivian squirrel monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.  
 OX NCBI\_TaxID=27679;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21265430; PubMed=11371582;  
 RA Liu J.C., Makova K.D., Adkins R.M., Gibson S., Li W.H.;  
 RT "Episodic Evolution of Growth Hormone in Primates and Emergence of the  
 RT Species Specificity of Human Growth Hormone Receptor.";  
 RL Mol. Biol. Evol. 18:945-953(2001).  
 DR EMBL; AF339061; AAK62288.1; -;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR002996; CRIA.  
 DR InterPro; IPR003961; FN.III.  
 DR InterPro; IPR003528; Hemtopoptn\_L\_F1.  
 DR Pfam; PF00041; fn3; 1.  
 DR SMART; SM00060; FN3; 1.  
 DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
 KW Receptor.  
 SQ SEQUENCE 632 AA; 70883 MW; 440E17AF6277EDA3 CRC64;  
 Query Match 88.4%; Score 38; DB 6; Length 632;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CEEDFY 6  
 Db 259 CEEDFY 264  
 RESULT 3  
 Q9XSZ1 PRELIMINARY; PRT; 638 AA.  
 AC Q9XSZ1;  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Growth hormone receptor.  
 OS Papio anubis (Olive baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Papio.  
 OX NCBI\_TaxID=9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99367319; PubMed=10425448;  
 RA Zogopoulos G., Nathanielsz P., Hendy G.N., Goodyer C.G.;  
 RT "The baboon: a model for the study of primate growth hormone receptor  
 RT gene expression during development.";  
 RL J. Mol. Endocrinol. 23:67-75(1999).  
 DR EMBL; AF150751; AAD39536.1; -;  
 DR HSP; P10912; IAXI.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR InterPro; IPR002996; CRIA.  
 DR InterPro; IPR003961; FN.III.  
 DR InterPro; IPR003528; Hemtopoptn\_L\_F1.  
 DR Pfam; PF00041; fn3; 1.  
 DR SMART; SM00060; FN3; 1.  
 DR PROSITE; PS01352; HEMATOPO\_REC\_L\_F1; 1.  
 KW Receptor.  
 SQ SEQUENCE 638 AA; 71407 MW; 9E2500C8E303E420 CRC64;  
 Query Match 88.4%; Score 38; DB 6; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 32;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CEEDFY 6  
 Db 259 CEEDFY 264  
 RESULT 4  
 Q8VCQ7 PRELIMINARY; PRT; 399 AA.  
 ID Q8VCQ7;  
 AC Q8VCQ7;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Open reading frame 6.  
 DE ORF6.  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC019440; AAH19440.1; -;  
 DR MGD; MGI:1352481; ORF6.  
 DR InterPro; IPR007529; Znf\_HIT.  
 DR Pfam; PF04438; zf-HIT; 1.  
 SQ SEQUENCE 399 AA; 42995 MW; B5CA88342B56932B CRC64;  
 Query Match 86.0%; Score 37; DB 11; Length 399;  
 Best Local Similarity 85.7%; Pred. No. 32;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 CEEDFYR 7  
 Db 41 CAEDFYR 47  
 RESULT 5  
 Q8C356 PRELIMINARY; PRT; 399 AA.  
 ID Q8C356;  
 AC Q8C356;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein.  
 GN ORF6.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Lung;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK086863; BAC39755.1; -;  
 DR MGD; MGI:1352481; ORF6.  
 DR InterPro; IPR007529; Znf\_HIT.  
 DR Pfam; PF04438; zf-HIT; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 399 AA; 42896 MW; F4CF854CSB5FEC87 CRC64;  
 Query Match 86.0%; Score 37; DB 11; Length 399;  
 Best Local Similarity 85.7%; Pred. No. 32;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CEEDFYR 7
Db 41 CAEDFYR 47

RESULT 6
Q9U9B1 PRELIMINARY; PRT; 76 AA.
ID Q9U9B1
AC Q9U9B1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ascaris type serine protease inhibitor (fragment).
OS Ancylostoma ceylanicum.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
OX NCBI_TaxID=53326;
RN [1]
RP SEQUENCE FROM N.A.
RA Harrison L.M., Cappello M.;
RT "The molecular cloning of an ascaris type serine protease inhibitor
from adult Ancylostoma ceylanicum hookworms.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172653; AAD51336.1; -.
DR HSP; P56682; 1CV.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01826; TIL; 1.
DR PROSITE; PS01186; EGF_2; 1.
KW Protease.
FT NON TER 1
SQ SEQUENCE 76 AA; 8385 MW; D35FCEF7C2088A53 CRC64;

Query Match 83.7%; Score 36; DB 5; Length 76;
Best Local Similarity 85.7%; Pred. No. 9.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
Db 44 CEEGFYR 50

RESULT 7
ID Q16938 PRELIMINARY; PRT; 91 AA.
AC Q16938;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Anti-coagulant protein C2 precursor (fragment).
OS Ancylostoma caninum (Dog hookworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
OX NCBI_TaxID=29170;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98298519; PubMed=8700900;
RA Jaspers L.S., Messens J.H., De Keyser A., Eeckhout D.,
RA van den Brande I., Gansemans Y.G., Lauwereys M.J., Vlaek G.P.,
RA Staussens P.E.;
RT "Surface expression and ligand-based selection of cDNAs fused to
filamentous phage gene VI.";
RL Biotechnology 13:378-382(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96312555; PubMed=8700900;
RA Staussens P., Bergum P.W., Gansemans Y., Jaspers L., Laroche Y.,
RA Huang S., Maki S., Messens J., Lauwereys M., Cappello M., Hotez P.J.,
RA Lasters I., Vlaek G.P.;
RT "Anticoagulant repertoire of the hookworm Ancylostoma caninum.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:2149-2154(1996).
DR EMBL; U30793; AAC47080.1; -.

PDB: 1COU; 13-OCT-99.
DR InterPro; IPR006209; EGF like.
DR Pfam; PF01826; TIL; 1.
DR PROSITE; PS01186; EGF_2; 1.
KW Signal.
FT NON TER 1
FT SIGNAL <1 7
FT CHAIN 8 91
SQ SEQUENCE 91 AA; 10358 MW; ECB11CB4597C24DA CRC64;
POTENTIAL.
ANTI-COAGULANT PROTEIN C2.

Query Match 83.7%; Score 36; DB 5; Length 91;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
Db 59 CEEGFYR 65

RESULT 8
Q98SF6 PRELIMINARY; PRT; 125 AA.
ID Q98SF6
AC Q98SF6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Lhx2 protein (fragment).
GN LHX2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RA Bachy I., Vernier P., Retaux S.;
RT "The LIM-homeodomain family in the developing xenopus brain:
conservation and divergences with the mouse related to the evolution
of the forebrain.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
IONS.
DR EMBL; AJ311712; CAC35215.1; -.
DR HSP; P32965; 1CTL.
DR InterPro; IPR001781; LIM.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000094; LIM; 1.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00478; LIM_DOMAIN 1; 1.
DR PROSITE; PS00023; LIM_DOMAIN 2; 2.
KW LIM domain; Metal-binding; Zinc.
FT NON TER 1
FT NON TER 125
SQ SEQUENCE 125 AA; 14283 MW; 375E42A29104D364 CRC64;

Query Match 83.7%; Score 36; DB 13; Length 125;
Best Local Similarity 71.4%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEEDFYR 7
Db 28 CKEDFYR 34

RESULT 9
Q14897 PRELIMINARY; PRT; 206 AA.
ID Q14897
AC Q14897;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

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DE L-myc protein (Similar to lung carcinoma myc related oncogene 1).  
GN L-MYC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=88094386; PubMed=2827002;  
RA Kaye F., Battey J., Nau M., Brooks B., Seifter E., De Greve J.,  
RA Birrer M., Sausville E., Minna J.;  
RT "Structure and expression of the human L-myc gene reveal a complex  
RT pattern of alternative mRNA processing.";  
RL Mol. Cell. Biol. 8:186-195(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; M19720; AAA59878.1; -;  
DR EMBL; BC011864; AAH11864.1; -;  
DR TRANSFAC; T02386; -;  
DR GO; GO:0005634; C:nucleus; NAS.  
DR GO; GO:0003700; F:transcription factor activity; NAS.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.  
DR InterPro; IPR002418; TF MYC.  
DR Pfam; PF01056; MYC N term; 1.  
DR PRINTS; PR00044; LEUZIPRMVC.  
DR SEQUENCE 206 AA; 21766 MW; 595C9CD6C9A8EC71 CRC64;  
SQ  
Query Match 83.7%; Score 36; DB 4; Length 206;  
Best Local Similarity 85.7%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CEEDFYR 7  
DB 15 CGEDFYR 21  
RESULT 10  
Q98SF7 PRELIMINARY; PRT; 217 AA.  
AC Q98SF7;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Lhx9 protein (Fragment).  
GN LHX9.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Head;  
RA Bachy I., Vernier P., Retaux S.;  
RT "The LIM-homeodomain family in the developing xenopus brain:  
RT conservation and divergences with the mouse related to the evolution  
RT of the forebrain.";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: CONTAINS 1 LIM DOMAIN. THE LIM DOMAIN BINDS 2 ZINC  
CC IONS.  
DR EMBL; AJ311171; CAC35214.1; -;  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR001781; LIM.  
DR Pfam; PF00046; homeobox; 1.  
DR Pfam; PF00412; LIM; 2.  
DR ProDom; PD000010; Homeobox; 1.

DR ProDom; PD000094; LIM; 2.  
DR SMART; SM00389; HOX; 1.  
DR SMART; SM00132; LIM; 1.  
DR PROSITE; PS50071; HOMEBOX 2; 1.  
DR PROSITE; PS00478; LIM DOMAIN 1; 1.  
DR PROSITE; PS50023; LIM DOMAIN 2; 1.  
KW LIM domain; Metal-binding; Zinc.  
FT NON\_TER 1  
FT NON\_TER 217  
SQ SEQUENCE 217 AA; 24716 MW; 6CBB88B595ECB851 CRC64;  
Query Match 83.7%; Score 36; DB 13; Length 217;  
Best Local Similarity 71.4%; Pred. No. 27;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CEEDFYR 7  
DB 27 CKEDYR 33  
RESULT 11  
Q811Z4 PRELIMINARY; PRT; 325 AA.  
ID Q811Z4  
AC Q811Z4;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE LIM-homeodomain type transcription factor Lhx9 (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Wistar;  
RA Mazaud S., Oreal E., Guigon C.J., Carre-Eusebe D., Magre S.;  
RT "Lhx9 expression during gonadal morphogenesis as related to the state  
RT of cell differentiation.";  
RL Gene Expr. Patterns 2:373-377(2002).  
DR EMBL; AF527619; AA027570.1; -;  
DR GO; GO:0005634; C:nucleus; IEA.  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR001356; Homeobox.  
DR InterPro; IPR001781; LIM.  
DR InterPro; IPR007107; LIM homeo.  
DR Pfam; PF00046; homeobox; 1.  
DR Pfam; PF00412; LIM; 2.  
DR ProDom; PD000010; Homeobox; 1.  
DR ProDom; PD000094; LIM; 2.  
DR SMART; SM00389; HOX; 1.  
DR SMART; SM00132; LIM; 2.  
DR PROSITE; PS00027; HOMEBOX 1; 1.  
DR PROSITE; PS50071; HOMEBOX 2; 1.  
DR PROSITE; PS00478; LIM DOMAIN 1; 2.  
DR PROSITE; PS50023; LIM DOMAIN 2; 2.  
KW Homeobox; DNA-binding; Nuclear protein.  
FT NON\_TER 1  
FT NON\_TER 325  
SQ SEQUENCE 325 AA; 36429 MW; CCA307A920FAB8AB CRC64;  
Query Match 83.7%; Score 36; DB 11; Length 325;  
Best Local Similarity 71.4%; Pred. No. 41;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CEEDFYR 7  
DB 89 CKEDYR 95  
RESULT 12  
Q865X9 PRELIMINARY; PRT; 369 AA.  
ID Q865X9





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RESULT 15
Q86UH2
ID Q86UH2 PRELIMINARY; PRT; 397 AA.
AC Q86UH2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LIM-homeobox 9 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Shan Y.X., Pan J., Guo Z.K., Geng D.C., Huang C.Q., Yu L.;
RT "Cloning and characterization of human novel LIM-homeobox 9 gene."
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY273889; AAP32471.2; -.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 397 AA; 43976 MW; FA8BBH550A5FCE03 CRC64;

Query Match      83.7%; Score 36; DB 4; Length 397;
Best Local Similarity 71.4%; Pred. No. 50;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CEDFYR 7
Db 120 CKEDYR 126

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Search completed: June 9, 2004, 15:51:24  
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